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(72) Inventeurs/Inventors:
BARRY, THOMAS GERARD, IE;
SMITH, TERENCE JAMES, IE
(73) Propriétaires/Owners:
ENTERPRISE IRELAND (TRADING AS BIORESEARCH
IRELAND), IE;
NATIONAL UNIVERSITY OF IRELAND, GALWAY, IE
(74) Agent: KIRBY EADES GALE BAKER

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ET EUCARYOTES
(54) Title: NUCLEIC ACID PROBE-BASED DIAGNOSTIC ASSAYS FOR PROKARYOTIC AND EUKARYOTIC
ORGANISMS

(57) **Abrégé/Abstract:**

Use of the *ssrA* gene or tmRNA, an RNA transcript of the *ssrA* gene, or fragments thereof as target regions in a nucleic acid probe assay for the detection and identification of prokaryotic and/or eukaryotic organisms is described. Nucleotide sequence alignment of tmRNA sequences from various organisms can be used to identify regions of homology and non-homology within the sequences which in turn can be used to design both genus specific and species specific oligonucleotide probes. These newly identified regions of homology and non-homology provide the basis of identifying and detecting organisms at the molecular level. Oligonucleotide probes identified in this way can be used to detect tmRNA in samples thereby giving an indication of the viability of non-viral organisms present in various sample types.



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(71) Applicants (for all designated States except US): **ENTERPRISE IRELAND** (trading as **BioResearch Ireland**) [IE/IE]; Glasnevin, Dublin 9 (IE). **NATIONAL UNIVERSITY OF IRELAND, GALWAY** [IE/IE]; University Road, Galway (IE).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **BARRY, Thomas, Gerard** [IE/IE]; The Quay, Kinvara, County Galway (IE). **SMITH, Terence, James** [IE/IE]; 18 Hawthorne Place, Clybaun Road, Galway (IE).

(74) Agent: **ANNE RYAN & CO.**; 60 Northumberland Road, Ballsbridge, Dublin 4 (IE).

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(54) Title: NUCLEIC ACID PROBE-BASED DIAGNOSTIC ASSAYS FOR PROKARYOTIC AND EUKARYOTIC ORGANISMS

(57) Abstract: Use of the *ssrA* gene or tmRNA, an RNA transcript of the *ssrA* gene, or fragments thereof as target regions in a nucleic acid probe assay for the detection and identification of prokaryotic and/or eukaryotic organisms is described. Nucleotide sequence alignment of tmRNA sequences from various organisms can be used to identify regions of homology and non-homology within the sequences which in turn can be used to design both genus specific and species specific oligonucleotide probes. These newly identified regions of homology and non-homology provide the basis of identifying and detecting organisms at the molecular level. Oligonucleotide probes identified in this way can be used to detect tmRNA in samples thereby giving an indication of the viability of non-viral organisms present in various sample types.

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DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
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CECI EST LE TOME __1__ DE __2__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __2__

NOTE: For additional volumes please contact the Canadian Patent Office.

Description

Nucleic acid probe-based diagnostic assays for prokaryotic and eukaryotic organisms.

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Technical Field

This invention relates to the identification of target sequences for use in nucleic acid assays for the detection and identification of prokaryotic and/or eukaryotic organisms.

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Background Art

The *ssrA* gene, which encodes a small stable high copy number RNA transcript (tmRNA), is found in all bacteria and has recently been identified in chloroplasts and diatoms. It has a dual function both as a tRNA and as an mRNA molecule and is involved in rescuing truncated mRNAs which have lost stop codons, facilitating trans-translation of truncated peptides prior to protease degradation (Keiler, K.C. *et al.* (1996), *Science*, 271, 990-993). The unique function of tmRNAs has directed researchers to analyse the relationship of the secondary structure of these molecules with their function. These studies have focussed on the conservation of the secondary structure of tmRNAs from different microorganisms, and on the evolutionary significance and functional relevance of such structural conservation. Studies were carried out by Matveeva, O *et al* (1998), Vol.

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16, No. 13, 1374-1375 to investigate oligonucleotide binding to RNA molecules using tmRNA as a model of RNA containing secondary structure. The studies did not have as their objective the identification of sites in tmRNA with the goal of designing antisense oligonucleotide for therapeutic purposes.

The number of nucleic acid targets/probes for bacterial diagnostics is currently limited. As such, the need to identify and characterise novel DNA and RNA targets for diagnostic purposes is now seen as a priority. Target nucleic acid sequences for the development of probes can be for example, plasmids, ribosomal RNA genes, intergenic regions, genes encoding virulence factors or random genomic DNA fragments. In addition, a number of RNA molecules have been described which are used as targets for RNA-based detection for example, ribosomal RNA and RNase P.

The basis of any nucleic acid-based probe assay is the requirement for well characterised nucleic acid sequences which are present in all prokaryotes and eukaryotes under study. For reliable detection of a prokaryotic or eukaryotic organism, the nucleic acid probes used should be highly specific (i.e. not cross-react with nucleic acids from other organisms) and highly sensitive (i.e. most or all strains of the organism to be detected should react with the probe). Therefore, preferred target sequences would be present in all strains of the organism concerned. Such sequences would have significant sequence variability to allow differentiation of the species concerned from other closely related species but, on the other hand, have

sufficient sequence conservation to allow the detection of all strains of the species concerned. In general, the precise identification of a nucleic acid sequence, which could form the basis of a specific nucleic acid probe assay, is tedious, difficult and uncertain. To date there are few general approaches
5 which would facilitate the development of nucleic acid probes for a wide variety of microorganisms. The nucleic acid sequences which have been identified as potentially useful targets for probe development are, for example, rRNA genes and RNA, and the rRNA 16S/23S intergenic region.

10 The majority of nucleic acid probe/target assays centre on the high copy number ribosomal RNAs (rRNA) and rRNA 16S/23S spacer regions (European Patent No. 0 395 292) of the bacterial cell for the purposes of detection and identification. A number of successful commercial bacterial diagnostic kits have been marketed based on these rRNA probes/targets for
15 the detection of a variety of microorganisms. These include a range of commercial probe kits based on the 16S rRNA gene marketed by Gen-probe Inc. San Diego California, and DNA probes based on the 16S/23S spacer region marketed by Innogenetics N.V. Ghent, Belgium. However, many of these diagnostic kits have limitations, including lack of sensitivity
20 due to low copy-number target sequences and lack of specificity due to sequence identity between closely related organisms in many cases.

Nucleic acid-based methods that could be applied directly to samples to give an indication of the viability of any microbes present therein would

be of enormous significance for food, industrial, environmental and medical applications.

5 A disadvantage of DNA-based methods is that they do not distinguish between living and dead organisms. Some studies have focussed on using rRNA and mRNA as indicators of cell viability (Sheridan, G.E.C. *et al.* (1998) *Applied and Environmental Microbiology*, 64, 1313-1318). However, these sequences are not satisfactory targets as rRNA and mRNA can be present in bacterial cells up to 48 hours after cell death.

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With the advent of nucleic acid based microarray-like formatting, incorporating simultaneous monitoring of multiple nucleic acid targets, there is now a clear requirement to identify and characterise novel nucleic acid sequences for use as probes and/or target regions to detect and identify
15 viable prokaryotic and eukaryotic cells.

Disclosure of Invention

Certain exemplary embodiments provide use of the *ssrA* gene or a
20 fragment thereof consisting of at least ten nucleotides as a target region in a nucleic acid probe assay for a prokaryotic or eukaryotic organism.

Certain other exemplary embodiments provide use of tmRNA, an RNA transcript of the *ssrA* gene, or a fragment thereof consisting of at least
25 ten nucleotides as a target region in a nucleic acid probe assay for a prokaryotic or eukaryotic organism.

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The invention provides use of the *ssrA* gene or a fragment thereof as a target region in a nucleic acid probe assay for a prokaryotic or eukaryotic organism.

5 Thus, the invention has application in relation to all organisms other than viruses.

No other nucleic acid probe assay has been reported which uses regions of the *ssrA* gene as a target region to detect and identify species of prokaryotes and eukaryotes with the attendant advantages.

5 According to one embodiment of the invention a fragment of the *ssrA* gene molecule corresponding to a region of high homology from the 5' end of the DNA molecule can be used as a universal target region.

10 In an alternative embodiment of the invention a fragment of the *ssrA* gene molecule corresponding to a region of high homology from the 3' end of the DNA molecule can be used as a universal target region.

15 In a further embodiment of the invention a fragment of the *ssrA* gene molecule corresponding to a region of low homology can be used as a target region in a nucleic acid probe assay to distinguish between species.

20 In a still further embodiment of the invention a fragment of the *ssrA* gene molecule corresponding to a region of low homology can be used as a target region for the generation of a genus specific probe.

25 As hereinafter described nucleotide sequence alignments of *ssrA* gene sequences from different organisms show that the 5' and 3' regions of these molecules demonstrate a high degree of homology and are therefore useful as universal target regions. The *ssrA* genes also demonstrate a more significant degree of nucleotide sequence variability between closely related

organisms than any other bacterial high copy number RNA. These variable regions are ideal targets for nucleic acid assays to distinguish between species.

5 The invention also provides use of tmRNA, an RNA transcript of the *ssrA* gene, or a fragment thereof as a target region in a nucleic acid probe assay for a prokaryotic or eukaryotic organism.

 According to one embodiment of this aspect of the invention a
10 fragment of a tmRNA molecule corresponding to a region of high homology from the 5' end of the tmRNA molecule can be used as a universal target region.

 Alternatively, a fragment of a tmRNA molecule corresponding to a
15 region of high homology from the 3' end of the tmRNA molecule can be used as a universal target region.

 According to a further embodiment of this aspect of the invention a
20 fragment of a tmRNA molecule corresponding to a region of low homology can be used as a target region in a nucleic acid probe assay to distinguish between species.

 According to a still further embodiment a fragment of a tmRNA
25 molecule corresponding to a region of low homology can be used as a target region for the generation of a genus specific probe.

The nucleic acid probe (DNA or RNA) in accordance with the invention typically consists of at least 10 nucleotides of the *ssrA* gene and / or tmRNA transcript or their complementary sequence and is used in a nucleic acid probe hybridisation assay for a prokaryotic or eukaryotic organism. Probe hybridisation to its complementary sequence is typically revealed by labelling the nucleic acid probe with a radioactive or non-radioactive (e.g. colorimetric or fluorimetric) label.

In preferred embodiments said *ssrA* gene fragment or said tmRNA fragment can be used as the basis of a primer to be used in an amplification procedure.

Universal oligonucleotide primers directed to the 5' and 3' regions of either the *ssrA* gene or the tmRNA sequence can be used in accordance with the invention to amplify the *ssrA* gene or its encoding tmRNA from a wide variety of bacteria, facilitating amplification of a wide range of organisms simultaneously, whilst also enabling specific nucleic acid probe hybridisation and detection.

Preferably, the product of the amplification procedure is used as a target region in a nucleic probe assay.

Further, preferably, a cDNA transcript of a tmRNA molecule is used as a probe in a nucleic acid hybridisation assay.

Such assays can be carried out *in vitro* or *in situ*.

The target region as defined herein can be used as the basis of an assay for distinguishing between living and dead prokaryotic or eukaryotic organisms.

In contrast to rRNA and mRNA which can be present in bacterial cells following cell death, tmRNA is rapidly degraded in dead organisms. Thus, tmRNA can be a useful target for distinguishing between living and dead prokaryotic or eukaryotic organisms either directly by nucleic acid probe hybridisation to isolated bacterial RNA, or by combined RNA amplification and nucleic acid probe hybridisation to the amplified product.

Preferably, the target region is used in a multiple probe format for broad scale detection and/or identification of prokaryotic or eukaryotic organisms.

An ssrA gene probe or a tmRNA transcript probe in accordance with the invention can be linked to a microarray gene chip system for the broad scale high throughput detection and identification of prokaryotic or eukaryotic organisms.

A target region in accordance with the invention can also be used as a probe in an assay to detect prokaryotic or eukaryotic organisms in a sample of matter.

Such a sample of matter can include biological samples such as samples of tissue from the respiratory tract, the uro-genital tract or the gastrointestinal tract, or body fluids such as blood and blood fractions,
5 sputum or cerebrospinal fluid.

An assay in accordance with the invention can also be carried out on food samples, environmental samples including air, water, marine and soil samples, and plant and animal derived samples.

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According to the invention a fragment of the *ssrA* gene or the tmRNA transcript can also be used in an assay to obtain a DNA profile of a prokaryotic or eukaryotic organism and, thereby, distinguish between strains of the same species.

15

Nucleic acid sequence alignments have shown that sequence variation occurs in the *ssrA* gene and the tmRNA transcript within individual species. This intra-species sequence variation can be used to distinguish between strains of the same species for epidemiology, tracing of
20 infectious agents for example, in outbreaks, or for population studies.

Other applications of the invention include the use of the *ssrA* gene, the tmRNA transcript or a DNA sequence complementary thereto, or a fragment thereof, to design an agent directed against infectious prokaryotic
25 or eukaryotic organisms for therapeutic purposes.

Such agents can include antisense mRNA or oligonucleotides, ribozymes, and antagonistic peptides and are suitable for use in any kind of medical condition.

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Thus, the invention can be used for the detection of viable organisms only in biological samples using the tmRNA target. Thus, during and following any anti-infectious agent drug treatment, the tmRNA target can be used to monitor the efficacy of the therapy on those specific infectious agents (e.g. antimicrobial and/or anti-parasitic treatments).

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In one embodiment, the target region is used to monitor the efficacy of drug therapies against infectious agents.

15

In another embodiment, the target region is used to monitor the viability and level of health-promoting organisms in the gastrointestinal tract.

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This aspect of the invention relates, for example, to the introduction into the gut flora of health-promoting (probiotic) organisms contained in for example yoghurt or other food to improve health. There is an interest and need to continuously monitor the presence and levels of these organisms to ensure their continued function in promoting health. The tmRNA region can be used as a target to detect viable organisms, for example in faeces, so as to monitor the presence of the health promoting organisms.

25

In a further embodiment, the assay is used for the quantification of prokaryotic or eukaryotic organisms.

5 When using probe hybridisation and/or *in vitro* amplification to detect organisms in a sample it is possible to determine the number of organisms present, based on the signal intensity. Real-time methods of *in vitro* amplification can also be used to enable the quantification of organisms in a sample. Thus, the ability to quantify the number of
10 organisms in a sample can be important in clinical situations for treatment purposes, for example for antibiotic or other treatments or for monitoring treatment efficacy.

 A still further application of the invention is the use of a database of
15 ssrA gene sequences to identify a prokaryotic or eukaryotic organism.

 The invention provides a variety of probes for the 5' and 3' homologous regions and the variable regions of the ssrA gene and tmRNA sequences, the probes being derived from these sequences or sequences
20 complementary thereto. Representative sequences are as follows:

Actinobacillus actinomycetemcomitans *ssrA*

GGGGCTGATTCTGGATTCGACGGGATTAGCGAAGCCCGAAGTGC
ACGTCGAGGTGCGGTAGGCCTCGTAAATAAACCGCAAAAAAATA
GTCGCAAACGACGAACAATACGCTTTAGCAGCTTAATAACCTGC
5 CTTTAGCCTTCGCTCCCCAGCTTCCGCTCGTAAGACGGGGATAAA
GCGGAGTCAAACCAAAACGAGATCGTGTGGAAGCCACCGTTTGA
GGATCGAAGCATTAAATTAAATCAAAGTAGCTTAATTGTCGCGT
GTCCGTCAGCAGGATTAAGTGAATTTAAAGACCGGACTAAACGT
GTAGTGCTAACGGCAGAGGAATTTTCGGACGGGGGTCAACTCCC
10 CCCAGCTCCACCA SEQ ID NO: 1

Actinobacillus actinomycetemcomitans tmRNA

GGGGCUGAUUCUGGAUUCGACGGGAUUAGCGAAGCCCGAAGU
GCACGUCGAGGUGCGGUAGGCCUCGUAAAUAACCGCAAAAAA
15 AUAGUCGCAAACGACGAACAUAACGCUUUAGCAGCUUAAUAAC
CUGCCUUUAGCCUUCGCUCCCCAGCUUCCGCUCGUAAAGACGGG
GAUAAAGCGGAGUCAAAACCAAAACGAGAUCGUGUGGAAGCCA
CCGUUUGAGGAUCGAAGCAUUAUUUUUUUCAAAGUAGCUUA
AUUGUCGCGUGUCCGUCAGCAGGAUUAAGUGAAUUUAAAGAC
20 CGGACUAAACGUGUAGUGCUAACGGCAGAGGAUUUUCGGACG
GGGGUUCAACUCCCCCCCAGCUCCACCA SEQ ID NO: 2

Aeromonas salmonicida ssrA, internal partial

AAGATTCACGAAACCCAAGGTGCATGCCGAGGTGCGGTAGGCCT
CGTTAACAAACCGCAAAAAAATAGTCGCAAACGACGAAAATA
CGCACTAGCAGCtTAATAACCTGCATAGAGCCCTTCTACCCTAGC
5 TTGCCTGTGTCCTAGGGAATCGGAAGGTCATCCTTCACAGGATC
GTGTGGAAGTCCTGCTCGGGGCGGAAGCATTAAAACCAATCGAG
CTAGTCAATTCGTGGCGTGTCTCTCCGCAGCGGGTTGGCGAATGT
AAAGAGTGACTAAGCATGTAGTACCGAGGATGTAGTAATTTTGG
ACGGGG SEQ ID NO: 3

10

Aeromonas salmonicida tmRNA, internal partial

AAGAUUCACGAAACCCAAGGUGCAUGCCGAGGUGCGGUAGGCC
UCGUUAACAAACCGCAAAAAAAUAGUCGCAAACGACGAAAACU
ACGCACUAGCAGCUUAAUAACCUGCAUAGAGCCCUUCUACCCU
15 AGCUUGCCUGUGUCCUAGGGAAUCGGAAGGUCAUCCUUCACAG
GAUCGUGUGGAAGUCCUGCUCGGGGCGGAAGCAUUA AAAACCA
AUCGAGCUAGUCAAUUCGUGGCGUGUCUCUCCGCAGCGGGUUG
GCGAAUGUAAAGAGUGACUAAGCAUGUAGUACCGAGGAUGUA
GUAAUUUUGGACGGGG SEQ ID NO: 4

20

Alcaligenes eutrophus ssrA

TGGGCCGACCTGGTTTCGACGTGGTTACAAAGCAGTGAGGCATA
CCGAGGACCCGTCACCTCGTTAATCAATGGAATGCAATAACTGC
TAACGACGAACGTTACGCACTCGCTTAATTGCGGCCGTCCTCGC
25 ACTGGCTCGCTGACGGGCTAGGGTCGCAAGACCACGCGAGGTAT

TTACGTCAGATAAGCTCCGGAAGGGTCACGAAGCCGGGGACGA
AAACCTAGTGACTCGCCGTCGTAGAGCGTGTTTCGTCCGATGCGC
CGGTAAATCAAATGACAGAACTAAGTATGTAGAACTCTCTGTG
GAGGGCTTACGGACGCGGGTTCGATTCCCGCCGGCTCCACCA
5 SEQ ID NO: 5

Alcaligenes eutrophus tmRNA

UGGGCCGACCUGGUUUCGACGUGGUUACAAAGCAGUGAGGCA
UACCGAGGACCCGUCACCUCGUUAAUCAAUUGGAAUGCAAUAAC
10 UGCUAACGACGAACGUUACGCACUCGCUUAAUUGCGGCCGUCC
UCGCACUGGCUCGCUGACGGGCUAGGGUCGCAAGACCACGCGA
GGUAUUUACGUCAGAUAAAGCUCCGGAAGGGUCACGAAGCCGG
GGACGAAAACCUAGUGACUCGCCGUCGUAGAGCGUGUUCGUCC
GAUGCGCCGGUUAUAAUCAAAUGACAGAACUAAGUAUGUAGAA
15 CUCUCUGUGGAGGGCUUACGGACGCGGGUUCGAUUCCCGCCGG
CUCCACCA SEQ ID NO: 6

Aquifex aeolicus ssrA

GGGGGCGGAAAGGATTCGACGGGGACAGGCGGTCCCCGAGGAG
20 CAGGCCGGGTGGCTCCCGTAACAGCCGCTAAACAGCTCCCGAA
GCTGAACTCGCTCTCGCTGCCTAATTAAACGGCAGCGCGTCCCC
GGTAGGTTTGCGGGTGGCCTACCGGAGGGGCGTCAGAGACACCCG
CTCGGGCTACTCGGTCGCACGGGGCTGAGTAGCTGACACCTAAC
CCGTGCTACCCTCGGGGAGCTTGCCCGTGGGCGACCCGAGGGGA

AATCCTGAACACGGGCTAAGCCTGTAGAGCCTCGGATGTGGCCG
CCGTCCTCGGACGCGGGTTCGATTCCCGCCGCCTCCACCA
SEQ ID NO: 7

5 *Aquifex aeolicus* tmRNA

GGGGGCGGAAAGGAUUCGACGGGGACAGGCGGUCCCCGAGGA
GCAGGCCGGGUGGCUCCCCGUAACAGCCGCUAAAACAGCUCCCCG
AAGCUGAACUCGCUCUCGCUGCCUAAUUAACGGCAGCGCGUC
CCCGGUAGGUUUGCGGGUGGCCUACCGGAGGGGCGUCAGAGACA
10 CCCGCUCGGGCUACUCGGUCGCACGGGGCUGAGUAGCUGACAC
CUAACCCGUGCUACCCUCGGGGAGCUUGCCCGUGGGGCGACCCG
AGGGGAAAUCCUGAACACGGGGCUAAGCCUGUAGAGCCUCGGAU
GUGGCCGCCGUCCUCGGACGCGGGUUCGAUUCCCGCCGCCUCC
ACCA SEQ ID NO: 8

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Bacillus megaterium ssrA, internal partial

AGGGTAGTTCGAGCTTAGGTTGCGAGTCGAGGAGATGGCCTCGT
TAAACATCAACGCCAATAATAACTGGCAAATCTAACAATAACT
TCGCTTTAGCTGCATAATAGTAGCTTAGCGTTCCTCCCTCCATCG
20 CCCATGTGGTAGGGTAAGGGACTCACTTTAAGTGGGCTACGCCG
GAGTTCGCCGTCTGAGGACGAAGGAAGAGAATAATCAGACTAG
CGACTGGGACGCCTGTTGGTAGGCAGAACAGCTCGCGAATGATC
AATATGCCAACTACACTCGTAGACGCTTAAGTGGCCATATTTCTG
GACGTGG SEQ ID NO: 9

25

Bacillus megaterium tmRNA, internal partial

AGGGUAGUUCGAGCUUAGGUUGCGAGUCGAGGAGAUGGCCUC
GUUAAAACAUCAACGCCAAUAAUAACUGGCAAAUCUAACAAU
AACUUCGCUUUAGCUGCAUAAUAGUAGCUUAGCGUUCCUCCCU
5 CCAUCGCCCAUGUGGUAGGGUAAGGGACUCACUUUAAGUGGGC
UACGCCGGAGUUCGCCGUCUGAGGACGAAGGAAGAGAAUAAU
CAGACUAGCGACUGGGACGCCUGUUGGUAGGCAGAACAGCUCG
CGAAUGAUCAAUAUGCCAACUACACUCGUAGACGCUUAAGUGG
CCAUAUUUCUGGACGUGG SEQ ID NO: 10

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Bacillus subtilis *ssrA*

GGGGACGTTACGGATTCGACAGGGATGGATCGAGCTTGAGCTGC
GAGCCGAGAGGGCGATCTCGTAAACACGCACTTAAATATAACTGG
CAAACCTAACAGTTTTAACC AAAACG TAGCATTAGCTGCCTAAT
15 AAGCGCAGCGAGCTCTTCCTGACATTGCCTATGTGTCTGTGAAG
AGCACATCCAAGTAGGCTACGCTTGCGTTCCCGTCTGAGAACGT
AAGAAGAGATGAACAGACTAGCTCTCGGAAGGCCCGCCCGCAG
GCAAGAAGATGAGTGAAACCATAAATATGCAGGCTACGCTCGTA
GACGCTTAAGTAATCGATGTTTCTGGACGTGGGTTCGACTCCCAC
20 CGTCTCCACCA SEQ ID NO: 11

Bacillus subtilis tmRNA

GGGGACGUUACGGAUUCGACAGGGAUGGAUCGAGCUUGAGCU
GCGAGCCGAGAGGGCGAUCUCGUAAACACGCACUUA AAUAUAAC
25 UGGCAAAACUAACAGUUUUAACCAAAACGUAGCAUUAGCUGCC

UAAUAAGCGCAGCGAGCUCUUCCUGACAUUGCCUAUGUGUCUG
UGAAGAGCACAUCCAAGUAGGCUACGCUUGCGUUCCCGUCUGA
GAACGUAAGAAGAGAUGAACAGACUAGCUCUCGGAAGGCCCGC
CCGCAGGCAAGAAGAUGAGUGAAACCAUAAAUAUGCAGGCUA
5 CGCUCGUAGACGCUUAAGUAAUCGAUGUUUCUGGACGUGGGU
UCGACUCCCACCGUCUCCACCA SEQ ID NO: 12

Bordetella pertussis *ssrA*

GGGGCCGATCCGGATTCTGACGTGGGTCATGAAACAGCTCAGGGC
10 ATGCCGAGCACCAGTAAGCTCGTTAATCCACTGGAACACTACAA
ACGCCAACGACGAGCGTCTCGCTCTCGCCGCTTAAGCGGTGAGC
CGCTGCACTGATCTGTCCTTGGGTCAGGCGGGGGAAGGCAACTT
CACAGGGGGCAACCCCGAACCGCAGCAGCGACATTCACAAGGA
ATCGGCCACCGCTGGGGGTCACACGGCGTTGGTTTAAATTACGTG
15 AATCGCCCTGGTCCGGCCCCGTCGATCGGCTAAGTCCAGGGTTAA
ATCCAAATAGATCGACTAAGCATGTAGAACTGGTTGCGGAGGGC
TTGCGGACGGGGGGTTCAATTCCCCCGGCTCCACCA
SEQ ID NO: 13

20 *Bordetella pertussis* tmRNA

GGGGCCGAUCCGGAUUCGACGUGGGUCAUGAAACAGCUCAGGG
CAUGCCGAGCACCAGUAAGCUCGUUAAUCCACUGGAACACUAC
AAACGCCAACGACGAGCGUCUCGCUCUCGCCGCUUAAGCGGUG
AGCCGCUGCACUGAUCUGUCCUUGGGUCAGGCGGGGGGAAGGCA
25 ACUUCACAGGGGGCAACCCCGAACCGCAGCAGCGACAUUCACA

AGGAAUCGGCCACCGCUGGGGUCACACGGCGUUGGUUUUAAAUU
ACGUGAAUCGCCCUGGUCCGGCCCGUCGAUCGGCUAAGUCCAG
GGUUAAAUCCAAAUAGAUCGACUAAGCAUGUAGAACUGGUUG
CGGAGGGGCUUGCGGACGGGGGUUCAAUUCCCCCGGCUCCACC
5 A SEQ ID NO: 14

Borrelia burgdorferi ssrA

GGGGATGTTTTGGATTTGACTGAAAATGTTAATATTGTAAGTTGC
AGGCAGAGGGAATCTCTTAAAACCTTCTAAAATAAATGCAAAAAA
10 TAATAACTTTACAAGCTCAAATCTTGTAATGGCTGCTTAAGTTAG
CAGAGGGTTTTGTTGAATTTGGCTTTGAGGTTCACTTATACTCTT
TTCGACATCAAAGCTTGCTTAAAAATGTTTTCAAGTTGATTTTAA
GGGACTTTTATACTTGAGAGCAATTTGGTGGTTTGCTAGTATTTC
CAAACCATATTGCTTAATAAAATACTAGATAAGCTTGTAGAAGC
15 TTATAGTATTATTTTAGGACGCGGGTTCAATTCCCGCCATCTCC
ACCA SEQ ID NO: 15

Borrelia burgdorferi tmRNA

GGGGAUGUUUUGGAUUUGACUGAAAAUGUUAUAUUGUAAGU
20 UGCAGGCAGAGGGAUUCUCUUAACUUCUAAAAUAAAUGCA
AAAAAUAUAACUUUACAAGCUCAAUUCUUGUAAUGGCUGCU
UAAGUUAGCAGAGGGUUUUGUUGAAUUUGGCUUUGAGGUUCA
CUUAUACUCUUUUCGACAUCAAAGCUUGC UUAAAAAUGUUUU
CAAGUUGAUUUUUAGGGACUUUUUAUACUUGAGAGCAAUUUGG
25 UGGUUUGCUAGUAUUUCCAAACCAUAUUGCUUAAUAAAAUAC

UAGAUAAAGCUUGUAGAAGCUUAUAGUAUUAUUUUUAGGACGC
GGGUUCAAUUCCCGCCAUCUCCACCA SEQ ID NO: 16

Campylobacter jejuni ssrA

5 GGGAGCGACTTGGCTTCGACAGGAGTAAGTCTGCTTAGATGGCA
TGTCGCTTTGGGCAAAGCGTAAAAAGCCCAAATAAAATTAAACG
CAAACAACGTTAAATTCGCTCCTGCTTACGCTAAAGCTGCGTAA
G TTCAGTTGAGCCTGAAATTTAAGTCATACTATCTAGCTTAATTT
TCGGTCATTTTTTGATAGTGTAGCCTTGCGTTTGACAAGCGTTGAG
10 GTGAAATAAAGTCTTAGCCTTGCTTTTGAGTTTTGGAAGATGAGC
GAAGTAGGGTGAAGTAGTCATCTTTGCTAAGCATGTAGAGGTCT
TTGTGGGATTATTTTTTGGACAGGGGTTCGATTCCCCTCGCTTCCA
CCA SEQ ID NO: 17

15 *Campylobacter jejuni tmRNA*

GGGAGCGACUUGGCUUCGACAGGAGUAAGUCUGCUUAGAUGG
CAUGUCGCUUUGGGCAAAGCGUAAAAAGCCCAAUAAAAUUA
AACGCAAACAACGUUAAAUUCGCUCCUGCUUACGCUAAAGCUG
CGUAAGUUCAGUUGAGCCUGAAAUUUAAGUCAUACUAUCUAG
20 CUUAAUUUUCGGUCAUUUUUGAUAGUGUAGCCUUGCGUUUGA
CAAGCGUUGAGGUGAAAUAAGUCUUAGCCUUGCUUUUGAGU
UUUGGAAGAUGAGCGAAGUAGGGUGAAGUAGUCAUCUUUGCU
AAGCAUGUAGAGGUCUUUGUGGGAUUAUUUUUGGACAGGGGU
UCGAUUCCCCUCGCUUCCACCA SEQ ID NO: 18

Chlamydia trachomatis (D/UW-3/CX) *ssrA*

GGGGGTGTAAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCAT
GCGGAGGGCGTTGGCTGGCCTCCTAAAAAGCCGACAAAACAATA
AATGCCGAACCTAAGGCTGAATGCGAAATTATCAGCTTCGCTGA
5 TCTCGAAGATCTAAGAGTAGCTGCTTAATTAGCAAAGTTGTTACC
TAAATACGGGTGACCCGGTGTTTCGCGAGCTCCACCAGAGGTTTT
CGAAACACCGTCATGTATCTGGTTAGAACTTAGGTCCTTTAATTC
TCGAGGAAATGAGTTTGAAATTTAATGAGAGTCGTTAGTCTCTAT
AGGGGTTTCTAGCTGAGGAGACATAACGTATAGTACCTAGGAAC
10 TAAGCATGTAGAGGTTAGCGGGGAGTTTACTAAGGACGAGAGTT
CGACTCTCTCCACCTCCACCA SEQ ID NO: 19

Chlamydia trachomatis (D/UW-3/CX) tmRNA

GGGGGUGUAAAGGUUUCGACUUAGAAAUGAAGCGUUAUUGC
15 AUGCGGAGGGCGUUGGCUGGCCUCCUAAAAAGCCGACAAAACA
AUAAAUGCCGAACCUAAGGCUGAAUGCGAAAUUAUCAGCUUC
GCUGAUCUCGAAGAUCUAAGAGUAGCUGCUUAAUUAGCAAAG
UUGUUACCUAAAUACGGGUGACCCGGUGUUCGCGAGCUCCACC
AGAGGUUUUCGAAACACCGUCAUGUAUCUGGUUAGAACUUAG
20 GUCCUUUAAUUCUCGAGGAAAUGAGUUUGAAAUUUAAUGAGA
GUCGUUAGUCUCUAUAGGGGUUUCUAGCUGAGGAGACAUAAC
GUAUAGUACCUAGGAACUAAGCAUGUAGAGGUUAGCGGGGAG
UUUACUAAGGACGAGAGUUCGACUCUCUCCACCUCACCA
SEQ ID NO: 20

Chlamydia trachomatis (mouse pneumonitis) *ssrA*

GGGGGTGTAAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCAT
GCGGAGGGCGTTGGCTGGCCTCCTAAAAAGCCGACAAAACAATA
AATGCCGAACCTAAGGCTGAATGCGAAATTATCAGCTTCGCTGA
5 TCTTAATGATCTAAGAGTTGCTGCTTAATTAGCAAAGTTGTTACC
TAAGTACTGGTAACCCGGTGTTTCGCGAGCTCCACCAGAGGTTTTTC
GAAACGCCGTCATTTATCTGGTTAGAATTAGGGCCTTTTAACTCT
CAAGGGAACTAATTTGAATTTTAATGAGAGTCGTTGGTCTCTATA
GAGGTTTCTAGCTGAGGAGATATAACGTAAAATATTCTAGAAAC
10 TAAGCATGTAGAGGTTAGCGGGGAGTTTACTAAGGACGAGAGTT
CGAATCTCTCCACCTCCACCA SEQ ID NO: 21

Chlamydia trachomatis (mouse pneumonitis) tmRNA

GGGGGUGUAAAGGUUUCGACUUAGAAAUGAAGCGUUAUUGC
15 AUGCGGAGGGCGUUGGCUGGCCUCCUAAAAAGCCGACAAAACA
AUAAAUGCCGAACCUAAGGCUGAAUGCGAAAUUAUCAGCUUC
GCUGAUCUUAUUGAUCUAAGAGUUGCUGCUUAAUUAGCAAAG
UUGUUACCUAAGUACUGGUAACCCGGUGUUCGCGAGCUCCACC
AGAGGUUUUCGAAACGCCGUCAUUUAUCUGGUUAGAAUUAGG
20 GCCUUUUUAAACUCUCAAGGGAACUAAUUUGAAUUUUAAUGAGA
GUCGUUGGUCUCUAUAGAGGUUUCUAGCUGAGGAGAUUAUAC
GUAAAUAUUCUAGAAACUAAGCAUGUAGAGGUUAGCGGGGA
GUUUACUAAGGACGAGAGUUCGAAUCUCUCCACCUCACCA
SEQ ID NO: 22

Chlorobium tepidum ssrA

GGGGATGACAGGCTATCGACAGGATAGGTGTGAGATGTCGTTGC
ACTCCGAGTTTCAGCATGGACGGACTCGTTAAACAAGTCTATGT
ACCAATAGATGCAGACGATTATTCGTATGCAATGGCTGCCTGAT
5 TAGCACAAGTTAATTCAGAAGCCATCGTCCTGCGGTGAATGCGC
TTACTCTGAAGCCGCCGGATGGCATAACCCGCGCTTGAGCCTAC
GGGTTCGCGCAAGTAAGCTCCGTACATTCATGCCCCGAGGGGGTG
TGCGGGTAACCAATCGGGATAAGGGGACGAACGCTGCTGGCGGT
GTAATCGGACCACGAAAAACCAACCACCAGAGATGAGTGTGGT
10 AACTGCATCGAGCAGTGTCTCTGGACGCGGGTTCAAGTCCCGCCA
TCTCCACCA SEQ ID NO: 23

Chlorobium tepidum tmRNA

GGGGAUGACAGGCUAUCGACAGGAUAGGUGUGAGAUGUCGUU
15 GCACUCCGAGUUUCAGCAUGGACGGACUCGUUAAACAAGUCUA
UGUACCAAUAGAUGCAGACGAUUAUUCGUAUGCAAUGGCUGC
CUGAUUAGCACAAAGUUAUUCAGAAGCCAUCGUCCUGCGGUGA
AUGCGCUUACUCUGAAGCCGCCGGAUGGCAUAACCCGCGCUUG
AGCCUACGGGUUCGCGCAAGUAAGCUCCGUACAUAUGCCCCG
20 AGGGGGUGUGCGGGUAACCAUUCGGGAUAAGGGGACGAACGC
UGCUGGCGGUGUAAUCGGACCACGAAAAACCAACCACCAGAGA
UGAGUGUGGUAACUGCAUCGAGCAGUGUCCUGGACGCGGGGUU
CAAGUCCCGCCAUCUCCACCA SEQ ID NO: 24

Cyanophora paradoxa (alga) cyanelle *ssrA*

GGGGCTGTTTAGGTTTCGACGTTTTTTTCTAATTATGTTTGTTAAG
CAAGTCGAGGATTTGTTCTATCTCGAAAATCAAGAACTCTCAAA
ATTTAAACGCAACTAATATTGTACGTTTTTAACCGTAAAGCAGCTT
5 TCGCTGTTTAATAATTACTTTTAATTTAAAAACCTAATTTTTTTTAG
GAATTTATTTATTTATTGTTTATCCTGCTTAATGAATTAAAAAAA
GCTATACTTGTGAATAAACGCATAATTTAAAAAAAACGGACGTGG
GTTCAAATCCCACCAGCTCCACCA SEQ ID NO: 25

10 *Cyanophora paradoxa* (alga) cyanelle tmRNA

GGGGCUGUUUAGGUUUCGACGUUUUUUUCUAAUUAUGUUUGU
UAAGCAAGUCGAGGAUUUGUUCUAUCUCGAAAAUCAAGAACU
CUCAAAAUUUAAACGCAACUAAUUAUUGUACGUUUUAACCGUA
AAGCAGCUUUCGCUGUUUAAUAAUUAUUAUUUUAUUUAAAAAC
15 CUAAUUUUUUUAGGAAUUUUAUUUUAUUUUAUUGUUUAUCCUGCU
UAAUGAAUUAUUUUUUUAGCUAUACUUGUGAAUAAACGCAUAAU
UUUUUUUUUACGGACGUGGGUUCAAAUCCCACCAGCUCCACCA
SEQ ID NO: 26

20 *Clostridium acetobutylicum* *ssrA*, 3' partial

AATCTGGCGTCGAGAGCGGGGAAACGAGCCTTACAAAGCTTTGA
GTAAGGAACGGAATTTATGAAGCTACTGAAGTGAAAAGCTTGTT
TGTAGGCGTTTCATGGAGGGAATGTTAAAATACAAACTGCACTC
GGAGATGCTTAATGAAACCATTTTCGGACAGGGGTTCGATTCCC
25 CTCGCCTCCACCA SEQ ID NO: 27

Clostridium acetobutylicum tmRNA, 3' partial

AAUCUGGCGUCGAGAGCGGGGAAACGAGCCUUACAAAGCUUU
GAGUAAGGAACGGAAUUUAUGAAGCUACUGAAGUGAAAAGCU
5 UGUUUGUAGGCGUUUCAUGGAGGGGAAUGUUAAAAUACAAACU
GCACUCGGAGAUGCUUAAUGAAACCAUUUUCGGACAGGGGGUU
CGAUUCCCCUCGCCUCCACCA SEQ ID NO: 28

Deinococcus radiodurans ssrA

10 GGGGGTGACCCGGTTTCGACAGGGGGAACCTGAAGGTGATGTTGCG
TGTCGAGGTGCCGTTGGCCTCGTAAACAAACGGCAAAGCCATTT
AACTGGCAACCAGAACTACGCTCTCGCTGCTTAAGTGAGATGAC
GACCGTGCAGCCCGGCCTTTGGCGTCGCGGAAGTCACTAAAAAA
GAAGGCTAGCCCAGGCGATTCTCCATAGCCGACGGCGAAACTTT
15 ATGGAGCTACGGCCTGCGAGAACCTGCCCACTGGTGAGCGCCGG
CCCGACAATCAAACAGTGGGATACACACGTAGACGCACGCTGGA
CGGACCTTTGGACGGCGGTTCGACTCCGCCCACCTCCACCA
SEQ ID NO: 29

20 *Deinococcus radiodurans* tmRNA

GGGGGUGACCCGGUUUCGACAGGGGGAACUGAAGGUGAUGUUG
CGUGUCGAGGUGCCGUUGGCCUCGUAAACAAACGGCAAAGCCA
UUUAACUGGCAACCAGAACUACGCUCUCGCUGCUUAAGUGAGA
UGACGACCGUGCAGCCCGGCCUUUGGCGUCGCGGAAGUCACUA
25 AAAAAGAAGGCUAGCCCAGGCGAUUCUCCAUAGCCGACGGCGA

AACUUUAUGGAGCUACGGCCUGCGAGAACCUGCCCACUGGUGA
GCGCCGGCCCGACAAUCAAACAGUGGGAUACACACGUAGACGC
ACGCUGGACGGACCUUUGGACGGCGGUUCGACUCCGCCCACCU
CCACCA SEQ ID NO: 30

5

Desulfovibrio desulfuricans *ssrA*, internal partial

GGGACTGGAACCGTAGCGGCAGGTCGAGGCGCCGCTGGCCTCGT
AAAAAGCGGCACAAAAGTAATTGCCAACAACGATTACGACTAC
GCTTACGCTGCCTAATAACAGCGAGGCAATGACCGTTTAACGGT
10 CGCGCCGATCAGGGCCATGCCTGATAACCCTGATTGGCGACACT
TATCAGGCTGGCGAAAACCGGCTCTCGCCGGGGTTTTTCGCGAG
GAGTTTACCGGCGGGATTGCTGCGTTGTGCCTGGTCAGGGGGCCA
ACAGCGCGGTGAAATACATACTTGACCTAAACCTGTAATGCTTC
GTGTGGAATGTTCTCGGACGGGG SEQ ID NO: 31

15

Desulfovibrio desulfuricans tmRNA, internal partial

GGGACUGGAACCGUAGCGGCAGGUCGAGGCGCCGCUGGCCUCG
UAAAAAGCGGCACAAAAGUAAUUGCCAACAACGAUUACGACU
ACGCUUACGCUGCCUAAUAACAGCGAGGCAAUGACCGUUUAAC
20 GGUCGCGCCGAUCAGGGCCAUGCCUGAUAACCCUGAUUGGCGA
CACUUAUCAGGCUGGCGAAAACCGGCUCUCGCCGGGGUUUUUC
GCGAGGAGUUUACCGGCGGGGAUUGCUGCGUUGUGCCUGGUCA
GGGGCCAACAGCGCGGUGAAAUACAUAACUUGACCUAAACCUGU
AAUGCUUCGUGUGGAAUGUUCUCGGACGGGG SEQ ID NO: 32

25

Dichelobacter nodosus *ssrA*, 3' partial

CTCGAGGTGCATGTCGAGAATGAGAGAATCTCGTTAAATACTTT
CAAAACTTATAGTTGCAAACGACGACAACACTACGCTTTAGCGGCT
TAATTCCCGCTTTCGCTTACCTAGATTTGTCTGTGGGTTTACCGTA
5 AGCGACATTAAACACAGAATCGCTGGTTAACGCGTCCGCTGTAA
TCGGTTAAATTAAGCGGAATCGCTTGTAATAATGCCTGAGCGTTG
GCTGTTTATGAGTTAAACCTAATTAAGTCTCTAAACATGTAGTA
CCAAAAGTTAAGGATTCGCGGACGGGGGGTTCAAATCCCCCGCC
TCCACCA SEQ ID NO: 33

10

Dichelobacter nodosus tmRNA, 3' partial

CUCGAGGUGCAUGUCGAGAAUGAGAGAAUCUCGUUAAAUACU
UUCAAAACUUAUAGUUGCAAACGACGACAACUACGCUUUAGCG
GCUUAAUUCCCGCUUUCGCUUACCUAGAUUUGUCUGUGGGUUU
15 ACCGUAAGCGACAUAACACAGAAUCGCUGGUUAACGCGUCCG
CUGUUAUUCGGUUAUUAAGCGGAAUCGCUUGUAAAAUGCC
UGAGCGUUGGCUGUUUAUGAGUUAUAAACCUAAUUAACUGCUCU
AAACAUGUAGUACCAAAAAGUUAAGGAUUCGCGGACGGGGGUU
CAAUCCCCCGCCUCCACCA SEQ ID NO: 34

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Enterococcus faecalis *ssrA*

GGGGGCGTTACGGATTCGACAGGCATAGTTGAGCTTGAATTGCG
TTTCGTAGGTTACGGCTACGTTAAAACGTTACAGTTAAATATAAC
TGCTAAAAACGAAAACAATTCTTTCGCTTTAGCTGCCTAAAAAC
25 CAGCTAGCGAAGATCCTCCCGGCATCGCCCATGTGCTCGGGTCA

GGGTCCTAATCGAAGTGGGATACGCTAAATTTTCCGTCTGTAAA
ATTAGAGGAGCTTACCAGACTAGCAATACAGAATGCCTGTCAC
TCGGCACGCTGTAAAGCGAACCTTTAAATGAGTGTCTATGAACG
TAGAGATTTAAGTGGCAATATGTTTGGACGCGGGTTCGACTCCC
5 GCCGTCTCCACCA SEQ ID NO: 35

Enterococcus faecalis tmRNA

GGGGGCGUUACGGAUUCGACAGGCAUAGUUGAGCUUGAAUUG
CGUUUCGUAGGUUACGGCUACGUUAAAACGUUACAGUUAAAU
10 AUAACUGCUAAAAACGAAAACAAUUCUUUCGCUUUAGCUGCCU
AAAAACCAGCUAGCGAAGAUCUCCCGGCAUCGCCCAUGUGCU
CGGGUCAGGGUCCUAAUCGAAGUGGGAUACGCUAAAUUUUUC
CGUCUGUAAAAUUUAGAGGAGCUUACCAGACUAGCAAUACAG
AAUGCCUGUCACUCGGCACGCUGUAAAGCGAACCUUUAAAUGA
15 GUGUCUAUGAACGUAGAGAUUUAAGUGGCAAUAUGUUUGGAC
GCGGGUUCGACUCCCGCCGUCUCCACCA SEQ ID NO: 36

Escherichia coli ssrA

GGGGCTGATTCTGGATTCGACGGGATTTGCGAAACCCAAGGTGC
20 ATGCCGAGGGGGCGGTTGGCCTCGTAAAAAGCCGCAAAAAATAGT
CGCAAACGACGAAAACACTACGCTTTAGCAGCTTAATAACCTGCTT
AGAGCCCTCTCTCCCTAGCCTCCGCTCTTAGGACGGGGATCAAG
AGAGGTCAAACCCAAAAGAGATCGCGTGGAAGCCCTGCCTGGG
GTTGAAGCGTTAAAACTTAATCAGGCTAGTTTGTAGTGGCGTGT
25 CCGTCCGCAGCTGGCAAGCGAATGTAAAGACTGACTAAGCATGT

AGTACCGAGGATGTAGGAATTTTCGGACGCGGGTTCAACTCCCCGC
CAGCTCCACCA SEQ ID NO: 37

Escherichia coli tmRNA

5 GGGGCUGAUUCUGGAUUCGACGGGAUUUGCGAAACCCAAGGU
GCAUGCCGAGGGGGCGGUUGGCCUCGUAAAAAGCCGCAAAAAAU
AGUCGCAAACGACGAAAACUACGCUUUAGCAGCUUAAUAACCU
GCUUAGAGCCCUCUCUCCCCUAGCCUCCGCUCUUAGGACGGGGA
UCAAGAGAGGUCAAACCCAAAAGAGAUCGCGUGGAAGCCCUGC
10 CUGGGGUUGAAGCGUUA AAAACUUA AU CAGGCUAGUUUGUUAG
UGGCGUGUCCGUCCGCAGCUGGCAAGCGAAUGUAAAGACUGAC
UAAGCAUGUAGUACCGAGGAUGUAGGAAUUUCGGACGCGGGU
UCAACUCCCGCCAGCUCCACCA SEQ ID NO: 38

15 *Haemophilus influenzae* ssrA

GGGGCTGATTCTGGATTTCGACGGGATTAGCGAAGCCCAAGGTGC
ACGTCGAGGTGCGGTAGGCCTCGTAAATAAACCGCAAAAAAATA
GTCGCAAACGACGAACAATACGCTTTAGCAGCTTAATAACCTGC
ATTTAGCCTTCGCGCTCCAGCTTCCGCTCGTAAGACGGGGATAAC
20 GCGGAGTCAAACCAAAAACGAGATCGTGTGGAAGCCACCGTTTGA
GGATCGAAGCACTAAATTGAATCAA ACTAGCTTAAGTTTAGCGT
GTCTGTCCGCATGCTTAAGTGAAATTAAAGACGAGACTAAACGT
GTAGTACTGAAGGTAGAGTAATTTTCGGACGGGGGGTTCAACTCCC
CCCAGCTCCACCA SEQ ID NO: 39

Haemophilus influenzae tmRNA

GGGGCUGAUUCUGGAUUCGACGGGAUUAGCGAAGCCCAAGGU
GCACGUCGAGGUGCGGUAGGCCUCGUAAAUAAACCGCAAAAAA
AUAGUCGCAAACGACGAACAAUACGCUUUAGCAGCUUAAUAAC
5 CUGCAUUUAGCCUUCGCGCUCCAGCUUCCGCUCGUAAGACGGG
GAUAACGCGGAGUCAAAACCAAAACGAGAUCGUGUGGAAGCCAC
CGUUUGAGGAUCGAAGCACUAAAUUGAAUCAAAACUAGCUUAA
GUUUAGCGUGUCUGUCCGCAUGCUUAAGUGAAAUUAAAGACG
AGACUAAACGUGUAGUACUGAAGGUAGAGUAAUUUCGGACGG
10 GGGUUCAACUCCCCCCCAGCUCCACCA SEQ ID NO: 40

Helicobacter pylori (ATCC 43504) *ssrA*, internal partial

AGATTTCTTGTCGCGCAGATAGCATGCCAAGCGCTGCTTGTA
ACAGCAACAAAAATAACTGTAAACAACACAGATTACGCTCCAGC
15 TTACGCTAAAGCTGCGTGAGTTAATCTCCTTTTGGAGCTGGACTG
ATTAGAATTTCTAGCGTTTTTAATCGCTCCATAACCTTAAGCTAGA
CGCTTTTAAAAGGTGGTTCGCCTTTTAAACTAAGAAACAAGAAC
TCTTGAAACTATCTTAAGGTTTTAGAAAGTTGGACCAGAGCTAGT
TTTAAGGCTAAAAACTAACCAATTTTCTAAGCATTGTAGAAGTTT
20 GTGTTTAGGGCAAGATTTTTTGGACTGGG SEQ ID NO: 41

Helicobacter pylori (ATCC 43504) tmRNA, internal partial

AGAUUUCUUGUCGCGCAGAUAGCAUGCCAAGCGCUGCUUGUAA
AACAGCAACAAAAAUAAACUGUAAACAACACAGAUUACGCUCCA
25 GCUUACGCUAAAGCUGCGUGAGUUAAUCUCCUUUUGGAGCUG

GACUGAUUAGAAUUUCUAGCGUUUUAUUCGCUCCAUAACCUU
AAGCUAGACGCUUUUAAAAGGUGGUUCGCCUUUUAAACUAAG
AAACAAGAACUCUUGAAACUAUCUUAAGGUUUUAGAAAGUUG
GACCAGAGCUAGUUUUAAGGCUAAAAACUAACCAAUUUUCUA
5 AGCAUUGUAGAAGUUUGUGUUUAGGGCAAGAUUUUUGGACUG
GG SEQ ID NO: 42

Helicobacter pylori (strain 26695) *ssrA*

GGGGCTGACTTGGATTTCGACAGATTTCTTGTCGCACAGATAGC
10 ATGCCAAGCGCTGCTTGTAACAGCAACAAAAATAACTGTAAA
CAACACAGATTACGCTCCAGCTTACGCTAAAGCTGCGTGAGTTA
ATCTCCTTTTGGAGCTGGACTGATTAGAATTTCTAGCGTTTTAAT
CGCTCCATAACCTTAAGCTAGACGCTTTTAAAAGGTGGTTCGCCT
TTTAAACTAAGAAACAAGAACTCTTGAAACTATCTCAAGGTTTT
15 AGAAAGTTGGACCAGAGCTAGTTTTTAAGGCTAAAAAACCAACCA
ATTTTCTAAGCATTGTAGAAGTTTGTGTTTAGGGCAAGATTTTGT
GACTGGGGTTCGATTCCCCACAGCTCCACCA SEQ ID NO: 43

Helicobacter pylori (strain 26695) tmRNA

20 GGGGCUGACUUGGAUUUCGACAGAUUUCUUGUCGCACAGAU
GCAUGCCAAGCGCUGCUUGUAAAACAGCAACAAAAAUAACUGU
AAACAACACAGAUUACGCUCCAGCUUACGCUAAAGCUGCGUGA
GUUAAUCUCCUUUUGGAGCUGGACUGAUUAGAAUUUCUAGCG
UUUUAUUCGCUCCAUAACCUUAAGCUAGACGCUUUUAAAAGG
25 UGGUUCGCCUUUUAAACUAAGAAACAAGAACUCUUGAAACUA

UCUCAAGGUUUUAGAAAGUUGGACCAGAGCUAGUUUUAAGGC
UAAAAACCAACCAAUUUUCUAAGCAUUGUAGAAGUUUGUGU
UUAGGGCAAGAUUUUUGGACUGGGGUUCGAUUCCCCACAGCUC
CACCA SEQ ID NO: 44

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Klebsiella aerogenes (NCTC 9528) *ssrA* , internal partial

GGGATTCGCGAAACCCAAGGTGCATGCCGAGGGGCGGTTGGCCT
CGTAAAAAGCCGCAAAAAAATAGTCGCAAACGACGAAAACCTAC
GCTTTAGCAGCTTAATAACCTGCTAAGAGCCCTCTCTCCCTAGCT
10 TCCGCTCCTAAGACGGGGAATAAAGAGAGGTCAAACCCAAAAG
AGATCGCGTGGAAGCCCTGCCTGGGGTTGAAGCGTTAAAACTAA
TCAGGCTAGTTTGTCTAGTGGCGTGTCCGTCCGCAGCTGGCCAGC
GAATGTAAAGACTGGACTAAGCATGTAGTGCCGAGGATGTAGGA
ATTTC SEQ ID NO: 45

15

Klebsiella aerogenes (NCTC 9528) tmRNA, internal partial

GGGAUUCGCGAAACCCAAGGUGCAUGCCGAGGGGCGGUUGGCC
UCGUAAAAAGCCGCAAAAAAAUAGUCGCAAACGACGAAAACU
20 ACGCUUUAGCAGCUUAAUAACCUGCUAAGAGCCCUCUCUCCCU
AGCUUCCGCUCCUAAGACGGGGAAUAAAGAGAGGUCAAACCCA
AAAGAGAUCGCGUGGAAGCCCUGCCUGGGGUUGAAGCGUUAA
AACUAAUCAGGCUAGUUUGUCAGUGGCGUGUCCGUCCGCAGCU
GGCCAGCGAAUGUAAAGACUGGACUAAGCAUGUAGUGCCGAG
25 GAUGUAGGAAUUUC SEQ ID NO: 46

Lactobacillus lactis (NCTC 662) *ssrA*, internal partial

AAGCACAGTTCGAGCTTGAATTGCGTTTCGTAGGTTACGTCTACG
TTAAAACGTTACAGTTAAATATAACTGCTAAAAACGAAAACAAC
TCTTACGCTTTAGCTGCCTAAAAACAGTTAGCGTAGATCCTCTCG
5 GCATCGCCCATGTGCTCGAGTAAGGGTCTCAAATTTAGTGGGAT
ACGTTAAACTTTTCCGTCTGTAAAGTTTAAAAGAGATCATCAGAC
TAGCGATACAGAATGCCTGTCACCTCGGCAAGCTGTAAAGCGAAA
CCTCAAATGAGTTGACTATGAACGTAGATTTTAAAGTGTCGATGT
GTTT SEQ ID NO: 47

10

Lactobacillus lactis (NCTC 662) tmRNA, internal partial

AAGCACAGUUCGAGCUUGAAUUGCGUUUCGUAGGUUACGUCU
ACGUUAAAACGUUACAGUUAAAUAUAACUGCUAAAAACGAAA
ACAACUCUUACGCUUUAGCUGCCUAAAAACAGUUAGCGUAGAU
15 CCUCUCGGCAUCGCCCAUGUGCUCGAGUAAGGGUCUCAAAUUU
AGUGGGAUACGUUAAACUUUUCGUCUGUAAAGUUUAAAAGA
GAUCAUCAGACUAGCGAUACAGAAUGCCUGUCACUCGGCAAGC
UGUAAAGCGAAACCUCAAAUGAGUUGACUAUGAACGUAGAUU
UUUAAGUGUCGAUGUGUUU SEQ ID NO: 48

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Legionella pneumophila ssrA, internal partial

GTGGGTTGCAAAACCGGAAGTGCGATGCCGAGAAGGAGATCTCTC
GTAAATAAGACTCAATTAAATATAAATGCAAACGATGAAAACCTT
TGCTGGTGGGGAAGCTATCGCTGCCTAATAAGCACTTTAGTTAA
25 ACCATCACTGTGTACTGGCCAATAAACCCAGTATCCCGTTTCGACC

GAGCCCGCTTATCGGTATCGAATCAACGGTCATAAGAGATAAGC
TAGCGTCCTAATCTATCCCGGGTTATGGCGCGAAACTCAGGGAA
TCGCTGTGTATCATCCTGCCCCGTCGGAGGAGCCACAGTTAAATTC
AAAAGACAAGGCTATGCATGTAGAGCTAAAGGCAGAGGACTTG
5 CGGACGCGG SEQ ID NO: 49

Legionella pneumophila tmRNA, internal partial

GUGGGUUGCAAAACCGGAAGUGCAUGCCGAGAAGGAGAUCUC
UCGUAAAUAAGACUCAAUUAAAUAUAAAUGCAAACGAUGAAA
10 ACUUUGCUGGUGGGGAAGCUAUCGCUGCCUAAUAAGCACUUU
AGUUAAACCAUCACUGUGUACUGGCCAAUAAACCCAGUAUCCC
GUUCGACCGAGCCCGCUUAUCGGUAUCGAAUCAACGGUCAUAA
GAGAUAAAGCUAGCGUCCUAAUCUAUCCCGGGUUAUGGCGCGAA
ACUCAGGGAAUCGCUGUGUAUCAUCCUGCCCGUCGGAGGAGCC
15 ACAGUUAAAUUCAAAGACAAGGCUAUGCAUGUAGAGCUAAA
GGCAGAGGACUUGCGGACGCGG SEQ ID NO: 50

Listeria grayi *ssrA*, internal partial

ACAGGGATAGGTCGAGCTTGAGTTGCGAGCCGGGGGGGATCGGCC
20 CGTCATCAACGTCAAAGCCAATAATAACTGGCAAACAAAACAAC
AATTTAGCTTTCGCTGCCTAATAGCAGTCTGAATAGCTGATCCTC
CGTGCATCACCCATGTGCTACGGTAAGGGTCTCACTTTTAAGTGG
GTTACGCTGGCTTATCTCCGTCTGGGGCAAACGAGAAGAGCATA
ATCAGACTAGCTAGATAGAGCCCTGACGCCGGGCAGACATCTAT

GCGAAATCCAAATACGGCAACTACGCTCGTAGATGCTCAAGTGC
CGATATTTCTGG SEQ ID NO: 51

Listeria grayi tmRNA, internal partial

5 ACAGGGAUAGGUCGAGCUUGAGUUGCGAGCCGGGGGGGAUCGG
CCCGUCAUCAACGUCAAAGCCAAUAAUAACUGGCAAACAAAAC
AACAAUUUAGCUUUCGCUGCCUAAUAGCAGUCUGAAUAGCUG
AUCCUCCGUGCAUCACCCAUGUGCUACGGUAAGGGUCUCACUU
UUAAGUGGGUUACGCUGGCUUAUCUCCGUCUGGGGCAAACGA
10 GAAGAGCAUAAUCAGACUAGCUAGAUAGAGCCCUGACGCCGGG
CAGACAUCUAUGCGAAAUCCAAAUACGGCAACUACGCUCGUAG
AUGCUC AAGUGCCGAUAUUUCUGG SEQ ID NO: 52

Listeria innocua ssrA, internal partial

15 ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGGATCGTCC
TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA
AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG
GGCTACACTAGTTAATCTCCGTCTGAGGTAAATAGAAGAGCTT
20 AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA
TGCGAAATGCTAATAACGGTGACTACGCTCGTAGATATTCAAGTG
CCGATATTTCTGG SEQ ID NO: 53

Listeria innocua tmRNA, internal partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGGAUCGU
CCUCGUUAUCAACGUCAAAGCCAAUAAUAAACUGGCAAAGAAAA
ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG
5 AUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGGUCUCACUC
UAAGUGGGGCUACACUAGUUAUAUCUCCGUCUGAGGUUAAAUAG
AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG
CUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGCUCGUA
GAUAUUCAAGUGCCGAUAUUUCUGG SEQ ID NO: 54

10

Listeria monocytogenes (NCTC 7973)*ssrA*, internal partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGGATCGTCC
TCGTTATCAACGTCAAAGCCAATAATACTGGCAAAGAAAAACA
AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
15 CCGTGCAATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG
GGCTACACTAGTTAATCTCCGTCTGGGGTTAAATAGAAGAGCTT
AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTA
TGCGAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTG
CCGATATTTCTGG SEQ ID NO: 55

20

Listeria monocytogenes (NCTC 7973)tmRNA, internal partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGGAUCGU
CCUCGUUAUCAACGUCAAAGCCAAUAAUAAACUGGCAAAGAAAA
ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG
25 AUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGGUCUCACUC

UAAGUGGGCUACACUAGUUAUUCUCCGUCUGGGGUUAAAUAG
AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG
CCGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGCUCGUA
GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 56

5

Listeria monocytogenes (NCTC 11994) *ssrA*, internal partial

CAAAGCCAATAATAACTGGCAAAGAAAAACAAAACCTAGCTTTC
GCTGCCTAATAAGCAGTAGCATAGCTGATCCTCCGTGCATCGCC
CATGTGCTACGGTAAGGGTCTCACTCTAAGTGGGCTACACTAGTT
10 AATCTCCGTCTGGGGTTAAATAGAAGAGCTTAATCAGACTAGCT
GAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCTAA
TACGGTGACTACGCTCGTAGATATTT SEQ ID NO: 57

Listeria monocytogenes (NCTC 11994) tmRNA, internal partial

15 CAAAGCCAAUAAUAAACUGGCAAAGAAAAACAAAACCUAGCUU
UCGCUGCCUAAUAAGCAGUAGCAUAGCUGAUCCUCCGUGCAUC
GCCCAUGUGCUACGGUAAGGGUCUCACUCUAAGUGGGGCUACAC
UAGUUAUUCUCCGUCUGGGGUUAAAUAGAAGAGCUUAAUCAG
ACUAGCUGAAUGGAAGCCUGUUACCGGGCCGAUGUUUAUGCG
20 AAAUGCUAAUACGGUGACUACGCUCGUAGAUUUU
SEQ ID NO: 58

Listeria murrayi ssrA, internal partial

ACAGGGATAGTTTCGAGCTTGAGTTGCGAGTCGGGGGGGATCGTCC
25 TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA

AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG
GGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTT
AATGAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA
5 TGCGAAATGCTAATACGGTGACTACGCTCGTAGATATTCAAGTG
CCGATATTTCTGG SEQ ID NO: 59

Listeria murrayi tmRNA, internal partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGGAUCGU
10 CCUCGUUAUCAACGUCAAAGCCAAUAAUAAACUGGCAAAGAAAA
ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG
AUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACUC
UAAGUGGGGCUACACUAGUUAUAUCUCCGUCUGAGGUUAAAUAG
AAGAGCUUAAUGAGACUAGCUGAAUGGAAGCCUGUUACCGGG
15 CUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGCUCGUA
GAUAUUCAAGUGCCGAUAUUUCUGG SEQ ID NO: 60

Listeria welshimeri ssrA, internal partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGGATCGTCC
20 TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA
AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG
GGCTACACTGGCTAATCTCCGTCTGAGGTTAGTTGGAAGAGCTT
AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTA

TGCGAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTG
CCGATATTTCTGG SEQ ID NO: 61

Listeria welshimeri tmRNA, internal partial

5 ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU
CCUCGUUAUCAACGUCAAAGCCAAUAAUAACUGGCAAAGAAAA
ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG
AUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACUC
UAAGUGGGGCUACACUGGCUAAUCUCCGUCUGAGGUUAGUUGG
10 AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG
CCGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGCUCGUA
GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 62

Marinobacter hydrocarbonoclasticus ssrA, internal partial

15 GCCGGTGACGAACCCTTGGGTGCATGCCGAGATGGCAGCGAATC
TCGTAAATCCAAAGCTGCAACGTAATAGTCGCAAACGACGAAAA
CTACGCACTGGCGGCGTAAGCCGTTCCAGTCGTCCTGGCTGAGG
CGCCTATAACTCAGTAGCAACATCCCAGGACGTCATCGCTTATA
GGCTGCTCCGTTCCACCAGAGCTCACTGGTGTTTCGGCTAAGATTAA
20 AGAGCTCGCCTCTTGCACCCTGACCTTCGGGTCGCTTGAGGTTAA
ATCAATAGAAGGACACTAAGCATGTAGACCTCAAGGCCTAGTGC
TGGCGGACGCGG SEQ ID NO: 63

Marinobacter hydrocarbonoclasticus tmRNA, internal partial

GCCGGUGACGAACCCUUGGGUGCAUGCCGAGAUGGCAGCGAAU
CUCGUAAAUCCAAAGCUGCAACGUAAUAGUCGCAAACGACGAA
AACUACGCACUGGGCGGCGUAAGCCGUUCCAGUCGUCCUGGCUG
5 AGGCGCCUAUAACUCAGUAGCAACAUCCCAGGACGUCAUCGCU
UAUAGGCUGCUCCGUUCACCAGAGCUCACUGGUGUUCGGCUAA
GAUUAAGAGCUCGCCUCUUGCACCCUGACCUUCGGGUCGCUU
GAGGUUAAAUCAAUAGAAGGACACUAAGCAUGUAGACCUCAA
GGCCUAGUGCUGGCGGACGCGG SEQ ID NO: 64

10

Mycobacterium avium ssrA, internal partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACTGA
CCACCGTAAGCGTCGTTGCAAATAGATAAGCGCCGATTCACATC
AGCGCGACTTACCTCTCGCTGCCTAAGCGACAGCTAGTCCGTCA
15 GCCCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTAGAGGG
ATCCACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCAACA
GCGACTGGGATCGTCATCCTGGCTTGTTTCGCGTGACCAGGAGAT
CCGAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG
GAATGCCGTAGAACCCGGGTTCGATTCCCAA SEQ ID NO: 65

20

Mycobacterium avium tmRNA, internal partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAACUG
ACCACCGUAAGCGUCGUUGCAAAUAGAUAAAGCGCCGAUUCACA
UCAGCGCGACUUACCUCUCGCUGCCUAAGCGACAGCUAGUCCG
25 UCAGCCCCGGGAACGCCCUAGACCCGGAGCCUGGCGUCAGCUAG

AGGGAUCCACCGAUGAGUUCGGUCGCGGGACUCAUCGGGACAC
CAACAGCGACUGGGGAUCGUCAUCCUGGCUUGUUCGCGUGACCA
GGAGAUCCGAGUAGAGGCAUAGCGAACUGCGCACGGAGAAGCC
UUGAGGGGAAUGCCGUAGAACCCGGGUUCGAUUCCTCAA

5 SEQ ID NO: 66

Mycobacterium bovis *ssrA*, internal partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGAG
ACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTACAT
10 CAGCGCGACTACGTCTCGCTGCCTAAGCGACGGCTAGTCTGTCA
GACCGGGGAACGCCCTCGGCCCCGGACCCTGGCATCAGCTAGAGGG
ATCCACCGATGAGTCCGGTCGCGGGGACTCCTCGGGACAACCACA
GCGACTGGGATCGTCATCTCGGCTAGTTCGCGTGACCGGGAGAT
CCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG
15 GAATGCCGTAGG SEQ ID NO: 67

Mycobacterium bovis tmRNA, internal partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAGAG
ACCACCGUAAGCGUCGUUGCGACCAAUAAGCGCCGAUUCACA
20 UCAGCGCGACUACGUCUCGCUGCCUAAGCGACGGCUAGUCUGU
CAGACCGGGGAACGCCCU CGGCCCCGGACCCUGGCAUCAGCUAGA
GGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUCGGGACAAC
CACAGCGACUGGGGAUCGUCAUCUCGGCUAGUUCGCGUGACCGG
GAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAGCCU
25 UGAGGGGAAUGCCGUAGG SEQ ID NO: 68

Mycobacterium leprae ssrA

GGGGCTGAAAGGTTTCGACTTCGCGCATCGAATCAAGGGAAGCG
TGCCGGTGCAGGCAAGAGACCACCGTAAGCGTCGTTGCAGCAAT
ATAAGCGCCGATTCATATCAGCGCGACTATGCTCTCGCTGCCTAA
5 GCGATGGCTAGTCTGTCAGACCGGGAACGCCCTCGTCCCGGAGC
CTGGCATCAGCTAGAGGGATCTACCGATGGGTTCGGTCGCGGGA
CTCGTCGGGACACCAACCGCGACTGGGATCGTCATCCTGGCTAG
TTCGCGTGATCAGGAGATCCGAGTAGAGGCATAGCGAACTACGC
ACGGAGAAGCCTTGAGGGAAATGCCGTAGGACCCGGGTTCGATT
10 CCCGGCAGCTCCACCA SEQ ID NO: 69

Mycobacterium leprae tmRNA

GGGGCUGAAAGGUUUCGACUUCGCGCAUCGAAUCAAGGGAAG
CGUGCCGGUGCAGGCAAGAGACCACCGUAAGCGUCGUUGCAGC
15 AAUAUAAGCGCCGAUUCAUAUCAGCGCGACUAUGCUCUCGCUG
CCUAAGCGAUGGCUAGUCUGUCAGACCGGGAACGCCCUCGUCC
CGGAGCCUGGCAUCAGCUAGAGGGAUCUACCGAUGGGGUUCGGU
CGCGGGACUCGUCGGGACACCAACCGCGACUGGGAUCGUCAUC
CUGGCUAGUUCGCGUGAUCAGGAGAUCCGAGUAGAGGCAUAG
20 CGAACUACGCACGGAGAAGCCUUGAGGGGAAAUGCCGUAGGACC
CGGGUUCGAUUCCCGGCAGCUCCACCA SEQ ID NO: 70

Mycobacterium paratuberculosis ssrA, internal partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACTGA
25 CCACCGTAAGCGTCGTTGCAAATAGATAAGCGCCGATTACATC

AGCGCGACTTACCTCTCGCTGCCTAAGCGACAGCTAGTCCGTCA
GCCCCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTAGAGGG
ATCCACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCAACA
GCGACTGGGATCGTCATCCTGGCTTGTTTCGCGTGACCAGGAGAT
5 CCGAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG
GAATGCCGTAGAACCCGGGTTCGATTCCCAA SEQ ID NO: 71

Mycobacterium paratuberculosis tmRNA, internal partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAACUG
10 ACCACCGUAAGCGUCGUUGCAAAUAGAUAAAGCGCCGAUUCACA
UCAGCGCGACUUACCUCUCGCUGCCUAAGCGACAGCUAGUCCG
UCAGCCCCGGGAACGCCCUAGACCCGGAGCCUGGCGUCAGCUAG
AGGGAUCCACCGAUGAGUUCGGUCGCGGGACUCAUCGGGACAC
CAACAGCGACUGGGGAUCGUCAUCCUGGCUUGUUCGCGUGACCA
15 GGAGAUCCGAGUAGAGGCAUAGCGAACUGCGCACGGAGAAGCC
UUGAGGGAAUGCCGUAGAACCCGGGUUCGAUUCCTCAA
SEQ ID NO: 72

Mycobacterium tuberculosis *ssrA*

GGGGCTGAACGGTTTCGACTTCGCGCATCGAATCAAGGGAAGCG
20 TGCCGGTGCAGGCAAGAGACCACCGTAAGCGTCGTTGCGACCAA
ATAAGCGCCGATTCACATCAGCGCGACTACGCTCTCGCTGCCTA
AGCGACGGCTAGTCTGTCAGACCGGGAACGCCCTCGGCCCGGAC
CCTGGCATCAGCTAGAGGGATCCACCGATGAGTCCGGTCGCGGG
25 ACTCCTCGGGACAACCACAGCGACTGGGATCGTCATCTCGGCTA

GTTCGCGTGACCGGGAGATCCGAGCAGAGGCATAGCGAACTGCG
CACGGAGAAGCCTTGAGGGAATGCCGTAGGACCCGGGTTCGATT
CCCGGCAGCTCCACCA SEQ ID NO: 73

5 *Mycobacterium tuberculosis* tmRNA

GGGGCUGAACGGUUUCGACUUCGCGCAUCGAAUCAAGGGAAGC
GUGCCGGUGCAGGCAAGAGACCACCGUAAGCGUCGUUGCGACC
AAAUAAAGCGCCGAUUCACAUCAGCGCGACUACGCUCUCGCUGC
CUAAGCGACGGCUAGUCUGUCAGACCGGGAACGCCCUCGGCCC
10 GGACCCUGGCAUCAGCUAGAGGGAUCCACCGAUGAGUCCGGUC
GCGGGACUCCUCGGGACAACCACAGCGACUGGGAUCGUCAUCU
CGGCUAGUUCGCGUGACCGGGAGA UCCGAGCAGAGGCAUAGCG
AACUGCGCACGGAGAAGCCUUGAGGGAAUGCCGUAGGACCCGG
GUUCGAUUCCCGGCAGCUCCACCA SEQ ID NO: 74

15

Mycoplasma capricolum ssrA

GGGGATGTCATGGATTTGACAGGATATCTTTAGTACATATAAGC
AGTAGTGTTGTAGACTATAAATACTACTAGGTTTAAAAAAACGC
AAATAAAAACGAAGAACTTTTGAAATGCCAGCATTTATGATGA
20 ATAATGCATCAGCTGGAGCAAACCTTTATGTTTGCTTAATAACTAC
TAGTTTAGTTATAGTATTTTCACGAATTATAGATATTTTAAGCTTT
ATTTATAACCGTATTACCCAAGCTTAATAGAATATATGATTGCAA
TAAATATATTTGAAATCTAATTGCAAATGATATTTAACCTTTAGT
TAATTTTAGTTAAATATTTTAATTAGAAAATTAACCTAACTGTAG

AAAGTATGTATTAATATATCTTGGACGCGAGTTCGATTCTCGCCA
TCTCCACCA SEQ ID NO: 75

Mycoplasma capricolum tmRNA

5 GGGGAUGUCAUGGAUUUGACAGGAUAUCUUUAGUACAUAUAA
GCAGUAGUGUUGUAGACUAUAAAUAUACUACUAGGUUUAAAAAA
ACGCAAAUAAAAACGAAGAAACUUUUUGAAAUGCCAGCAUUUA
UGAUGAAUAAUGCAUCAGCUGGAGCAAACUUUAUGUUUGCUU
AAUAACUACUAGUUUAGUUUAUAGUAUUUCACGAAUUUAUAGAU
10 AUUUUAAGCUUUUAUUUAUAACCGUAUUACCCAAGCUUAAUAG
AAUAUAUGAUUGCAAUAAAUAUAUUUGAAAUCUAAUUGCAA
UGAUUUUAACCUUUAGUUAAUUUUAGUUAAAUAUUUUAAUU
AGAAAUAUAAACUAAACUGUAGAAAGUAUGUAUUAAUAUAUCU
UGGACGCGAGUUCGAUUCUCGCCAUCUCCACCA SEQ ID NO: 76

15

Mycoplasma genitalium (ATTC 33530, #1) *ssrA*

GGGGATGTTTTGGGTTTGACATAATGCTGATAGACAAACAGTAG
CATTGGGGTATGCCCCTTACAGCGCTAGGTTCAATAACCGACAA
AGAAAATAACGAAGTGTTGGTAGAACCAAATTTGATCATTAACC
20 AACAAGCAAGTGTTAACTTTGCTTTTGCATAAGTAGATACTAAA
GCTACAGCTGGTGAATAGTCATAGTTTGCTAGCTGTCATAGTTTA
TGACTCGAGGTAAATCGTTCAATTTAACCTTTAAAAATAGAACT
TGTTGTTTCCATGATTGTTTTGTGATCAATTGGAAACAAGACAAA
AATCCACAAAACATAAAATGTAGAAGCTGTTTGTTGTGTCCTTTAT
25 GGAAACGGGTTCGATTCCCGTCATCTCCACCA SEQ ID NO: 77

Mycoplasma genitalium (ATTC 33530, #1) tmRNA

GGGGAUGUUUUGGGUUUGACAUAUAUGCUGAUAGACAAACAGU
AGCAUUGGGGGUAUGCCCCUACAGCGCUAGGUUCAAUAACCGA
CAAAGAAAAUAACGAAGUGUUGGUAGAACC AAAUUUGAUCAU
5 UAACCAACAAGCAAGUGUUAACUUUGCUUUUGCAUAAGUAGA
UACUAAAGCUACAGCUGGUGAAUAGUCAUAGUUUGCUAGCUG
UCAUAGUUUAUGACUCGAGGUUAAAUCGUUCAAUUUUAACCUU
UAAAAAUAGAACUUGUUGUUUCCAUGAUUGUUUUGUGAUCAA
UUGGAAACAAGACAAAAAUCCACAAAACUAAAAUGUAGAAGC
10 UGUUUGUUGUGUCCUUUAUGGAAACGGGUUCGAUUCCCGUCA
UCUCCACCA SEQ ID NO: 78

Mycoplasma genitalium (ATTC 33530, #2) tmRNA, internal partial

ACATAATGCTGATAGACAAACAGTAGCATTGGGGGTATGCCCCTT
15 ACAGCGCTAGGTTCAATAACCGACAAAGAAAATAACGAAGTGTT
GGTAGATCCAAATTTGATCATTAACCAACAAGCAAGTGTTAACT
TTGCTTTTGCATAAGTAGATACTAAAGCTACAGCTGGTGAATAGT
CATAGTTTGCTAGCTGTCATAGTTTATGACTCGAGGTAAATCGT
TCAATTTAACCTTTAAAAATAGAACTTGTTGTTTCCATGATTGTT
20 TTGTGATCAATTGGAAACAAGACAAAATCCACAAAACCTAAAAT
GTAGAAGCTGTTTGTTGTGTCCTTTATGGAAACGGGTTC
SEQ ID NO: 79

Mycoplasma genitalium (ATTC 33530, #2) tmRNA, internal partial

ACAUAAUGCUGAUAGACAAACAGUAGCAUUGGGGUAUGCCCC
UUACAGCGCUAGGUUCAUAACCGACAAAGAAAAUAACGAAG
UGUUGGUAGAUCCAAAUUUGAUCAUUAACCAACAAGCAAGUG
5 UUAACUUUGCUUUUGCAUAAGUAGAUACUAAAGCUACAGCUG
GUGAAUAGUCAUAGUUUGCUAGCUGUCAUAGUUUAUGACUCG
AGGUUAAAUCGUUCAAUUUAACCUUUAAAAAUAGAACUUGUU
GUUUCCAUGAUUGUUUUUGUGAUCAAUUGGAAACAAGACAAAA
AUCCACAAAACUAAAAUGUAGAAGCUGUUUGUUGUGUCCUUU
10 AUGGAAACGGGUUC SEQ ID NO: 80

Mycoplasma pneumophila *ssrA*

GGGGATGTAGAGGTTTTGACATAATGTTGAAAGGAAAACAGTTG
CAGTGGGGTATGCCCCTTACAGCTCTAGGTATAATAACCGACAA
15 AAATAACGACGAAGTTTTGGTAGATCCAATGTTGATCGCTAACC
ACAAGCAAGTATCAACTACGCTTTCGCTTAGAACATACTAAAG
CTACACGAATTGAATCGCCATAGTTTGGTTCGTGTCACAGTTTAT
GGCTCGGGGTAACTGGTTCAACTTAATCCTTAAATTATGAACTT
ATCGTTTACTTGTTTGTCTTATGATCTAAAGTAAGCGAGACATTA
20 AAACATAAGACTAAACTGTAGAAGCTGTTTTACCAATCCTTTATG
GAAACGGGTTCGATTCCCGTCATCTCCACCA SEQ ID NO: 81

Mycoplasma pneumophila tmRNA

GGGGAUGUAGAGGUUUUGACAUA AUGUUGAAAGGAAAACAGU
25 UGCAGUGGGGUAUGCCCCUACAGCUCUAGGUUAUAUAACCGA

CAAAAUAACGACGAAGUUUUGGUAGAUCCAAUGUUGAUCGC
UAACCAACAAGCAAGUAUCAAACUACGCUUUCGCUUAGAACAU
CUAAAGCUACACGAAUUGAAUCGCCAUAGUUUGGUUCGUGUC
ACAGUUUAUGGCUCGGGGUUAACUGGUUCAACUAAUCCUUA
5 AAUUAUGAACUUAUCGUUUACUUGUUUGUCUUAUGAUCUAAA
GUAAGCGAGACAUUAAAACAUAAGACUAAACUGUAGAAGCUG
UUUUACCAAUCCUUUAUGGAAACGGGUUCGAUUCCCGUCAUCU
CCACCA SEQ ID NO: 82

10 *Neisseria gonorrhoeae* (ATCC 19424) *ssrA*, internal partial
GGGGGTGCGAAGCAGATGCGGGCATACCGGGGTCTCAGATTCC
CGTAAACACTGAATTCAAATAGTCGCAAACGACGAAACTTACG
CTTTAGCCGCTTAAGGCTAGCCGTTGCAGCAGTCGGTCAATGGG
CTGTGTGGCGAAAGCCACCGCAACGTCATCTTACATTGACTGGTT
15 TCCAGCCGGGTACTTGGCAGGAAATAAGACTTAAGGTAACTGG
TTTCCAAAAGGCCTGTTGGTCGGCATGATGGAAATAAGATTTTC
AAATAGACACAATAAGTATGTAGAACGCTTTGTAGAGGACTTT
CGGACGGGG SEQ ID NO: 83

20 *Neisseria gonorrhoeae* (ATCC 19424) tmRNA, internal partial
GGGGGUUGCGAAGCAGAU GCGGGCAUACCGGGGUCUCAGAUU
CCCGUAAAACACUGAAUUCAAAUAGUCGCAAACGACGAAACUU
ACGCUUUAGCCGCUUAAGGCUAGCCGUUGCAGCAGUCGGUCAA
UGGGCUGUGUGGCGAAAGCCACCGCAACGUCAUCUUA CAUUGA
25 CUGGUUUCAGCCGGGUUACUUGGCAGGAAAUAAGACUUAAG

GUAACUGGUUUCCAAAGGCCUGUUGGUCGGCAUGAUGGAAA
UAAGAUUUUCAAUAGACACAACUAAGUAUGUAGAACGCUUU
GUAGAGGACUUUCGGACGGGG SEQ ID NO: 84

5 *Neisseria gonorrhoeae* (FA 1090) *ssrA*

GGGGGCGACCTTGGTTTCGACGGGGGTTGCGAAGCAGATGCGGG
CATACCGGGGTCTCAGATTCCCGTAAAACACTGAATTCAAATAG
TCGCAAACGACGAAACTTACGCTTTAGCCGCTTAAGGCTAGCCG
TTGCAGCAGTCGGTCAATGGGCTGTGTGGTGAAAGCCACCGCAA
10 CGTCATCTTACATTGACTGGTTTCCAGCCGGGTTACTTGGCAGGA
AATAAGACTTAAGGTAACTGGTTTCCAAAAGGCCTGTTGGTCGG
CATGATGGAAATAAGATTTTCAAATAGACACAATAAGTATGTA
GAACGCTTTGTAGAGGACTTTCGGACGGGGGGTTCGATTCCCCC
GCCTCCACCA SEQ ID NO: 85

15

Neisseria gonorrhoeae (FA 1090) tmRNA

GGGGGCGACCUUGGUUUCGACGGGGGUUGCGAAGCAGAUGCG
GGCAUACCGGGGUCUCAGAUUCCCGUAAAACACUGAAUUCAAA
UAGUCGCAAACGACGAAACUUACGCUUUAGCCGCUUAAGGCUA
20 GCCGUUGCAGCAGUCGGUCA AUGGGCUGUGUGGUGAAAGCCAC
CGCAACGUCAUCUUACA UUGACUGGUUUCAGCCGGGUUACUU
GGCAGGAAAUAAAGACUUAAGGUAACUGGUUUCCAAAGGCCU
GUUGGUCGGCAUGAUGGAAAUAAAGAUUUUCAAUAGACACAA
CUAAGUAUGUAGAACGCUUUGUAGAGGACUUUCGGACGGGGG
25 UUCGAUUCGGGGGGGCCUCCACCA SEQ ID NO: 86

Neisseria meningitidis *ssrA*

GGGGGCGACCTTGGTTTCGACGGGGGTTGCGAAGCAGATGCGGG
CATACCGGGGTCTCAGATTCCCGTAAAACACTGAATTCAAATAG
TCGCAAACGACGAAACTTACGCTTTAGCCGCTTAAGGCTAGCCG
5 TTGCAGCAGTCGGTCAATGGGCTGTGTGGCGAAAGCCACCGCAA
CGTCATCTTACATTGACTGGTTTCCTGCCGGGGTTATTTGGCAGGA
AATGAGATTTAAGGTAACTGGTTTCCAAAAGGCCTGTTGGTCGG
CATGATGGAAATAAGATTTTCAAATAGACACAATAAGTATGTA
GAACGCTTTGTAGAGGACTTTCGGACGGGGGTTTCGATTCCCCC
10 GCCTCCACCA SEQ ID NO: 87

Neisseria meningitidis tmRNA

GGGGGCGACCUUGGUUUCGACGGGGGUUGCGAAGCAGAUGCG
GGCAUACCGGGGUCUCAGAUUCCCGUAAAACACUGAAUUCAAA
15 UAGUCGCAAACGACGAAACUUACGCUUUAGCCGCUUAAGGCUA
GCCGUUGCAGCAGUCGGUCA AUGGGCUGUGUGGGCGAAAGCCAC
CGCAACGUCAUCUUACA UUGACUGGUUUCCUGCCGGGUUAUUU
GGCAGGAAAUGAGAUUUUAAGGUAACUGGUUUCCAAAAGGCCU
GUUGGUCGGCAUGAUGGAAAUAAGAUUUUCAA AUAGACACAA
20 CUAAGUAUGUAGAACGCUUUGUAGAGGACUUUCGGACGGGGG
UUCGAUUCGGGGGGGCCUCCACCA SEQ ID NO: 88

Nostoc muscorum PCC7120 *ssrA*

GGGTCCGTCGGTTTCGACAGGTTGGCGAACGCTACTCTGTGATTC
25 AGGTCGAGAGTGAGTCTCCTCTGCAAATCAAGGCTCAAAACAAA

AGTAAATGCGAATAACATCGTTAAATTTGCTCGTAAGGACGCTC
TAGTAGCTGCCTAAATAGCCTCTTTCAGGTTTCGAGCGTCTTCGGT
TTGACTCCGTTAAGGACTGAAGACCAACCCCCAACGGATGCTCT
AGCAATGTTCTCTGGTTGGCTTGCTAGCTAAGATTTAATCAGAGC
5 ATCCTACGTTTCGGGATAATGAACGATTCCCGCCTTGAGGGGTCAG
AAAGGCTAAACCTGTGAATGAGCGGGGGGTCAATACCCAATTTG
GACAGCAGTTCGACTCTGCTCGATCCACCA SEQ ID NO: 89

Nostoc muscorum PCC7120 tmRNA

10 GGGUCCGUCGGUUUCGACAGGUUGGCGAACGCUACUCUGUGAU
UCAGGUCGAGAGUGAGUCUCCUCUGCAAAUCAAGGCUCAAAAC
AAAAGUAAAUGCGAAUAACAUCGUUAAAUUUGCUCGUAAGGA
CGCUCUAGUAGCUGCCUAAAUAGCCUCUUUCAGGUUCGAGCGU
CUUCGGUUUGACUCCGUUAAGGACUGAAGACCAACCCCCAACG
15 GAUGCUCUAGCAAUGUUCUCUGGUUGGCUUGCUCUAGCUAAGAU
UUAUCAGAGCAUCCUACGUUCGGGAUAAUGAACGAUUCCCGC
CUUGAGGGUCAGAAAGGCUAAACCUGUGAAUGAGCGGGGGGU
CAAUACCCA AUUUGGACAGCAGUUCGACUCUCGCUCAUCCACC
A SEQ ID NO: 90

20

Odontella sinensis (diatom) chloroplast *ssrA*

GGGGCTGACTTGGTTTCGACATTTAAAAATTGTTACAGTATGATG
CAGGTCGAAGTTTCTAATCTTCGTAAAAAAGAGAAATTTATAA
TAAATGCTAATAATTTAATTTCTTCTGTGTTTAAAAGTTTATCAA
25 CTAAGCAAAATAGTTTAAATTTAAGTTTTGCTGTTTAAGTTTTAT

GCACATTTAATGATCTAGTAAATAACTTTGTTCGCTATAATTTAT
ATTTATAACTAGACTTTTGTCTTTTTTATAGTTTAGAATAACTTTA
TCATTTCAAACCTCGTTCCATCTAGTTGAACTAAACCTGTGAACG
AATACTATAATAAAAATTTTTAGATGGACGTGGGTTCGACTCCCAT
5 CAGCTCCACCA SEQ ID NO: 91

Odontella sinensis (diatom) chloroplast tmRNA

GGGGCUGACUUGGUUUCGACAUUUAAAAAUUGUUACAGUAUG
AUGCAGGUCGAAGUUUCUAAUCUUCGUAAAAAAGAGAAAUU
10 UAUAAUAAAUGCUAAUAAUUUAAUUUCUUCUGUGUUUAAAAG
UUUAUCAACUAAGCAAAAUAGUUUAAAUUUUAAGUUUUGCUGU
UUAAGUUUUAUGCACAUUUAAUGAUCUAGUAAAUAACUUUGU
UCGCUAUAAUUUAUAUUUAUAACUAGACUUUUGUCUUUUUUA
UAGUUUAGAAUAACUUUAUCAUUUCAAACCUCGUUCCAUCUA
15 GUUGAACUAAACCUGUGAACGAAUACUAUAAUAAAAUUUUUA
GAUGGACGUGGGUUCGACUCCCAUCAGCUCCACCA
SEQ ID NO: 92

Porphyra purpureum (red alga) chloroplast *ssrA*

GGGGCTGCAAGGTTTCTACATTGTGAAAAACAAATATATGAAA
20 GTAAAACGAGCTCATTATTAGAGCTTTTAGTTAAATAAATGCAG
AAAATAATATTATTGCTTTTTCTCGAAAATTAGCTGTTGCATAAA
TAGTCTCAATTTTTGTAAATTCGAAGTGATAGACTCTTATACACTA
CGAATATTCTGTTAGAGTTGCTCTTAATAAAAGAAAAGTAAAAA
25 AATACAAATTCTTATGTTTTTTACCTGAATTGATTCAATTTAAGG

TTAGTATTTTTTTGATTTTTACAATGGACGTGGGTTCAAGTCCCAC
CAGCTCCACCA SEQ ID NO: 93

Porphyra purpureum (red alga) chloroplast tmRNA

5 GGGGCUGCAAGGUUUCUACAUUGUGAAAAACAAUAUAUGA
AAGUAAAACGAGCUCAUUAUUAGAGCUUUUAGUUAAAUAUAAU
GCAGAAAUAUAUAUUAUUGCUUUUUCUCGAAAUAUAGCUGUU
GCAUAAAUAAGUCUCAAUUUUUGUAAUUCGAAGUGAUAGACUC
UUAUACACUACGAAUAUUCUGUUAGAGUUGCUCUUAUAUAAA
10 GAAAAGUAAAAAAAAUAUCAAUUCUUAUGUUUUUUUACCUGAAU
UGAUUCAAUUUAAGGUUAGUAUUUUUUGAUUUUUUACAAUGGA
CGUGGGUUCAAGUCCCACCAGCUCCACCA SEQ ID NO: 94

Porphyromonas gingivalis ssrA

15 GGGGCTGACCGGCTTTGACAGCGTGATGAAGCGGTATGTAAGCA
TGTAGTGCGTGGGTGGCTTGCCTATAATCTCAGACATCAAAAG
TTTAATTGGCGAAAATAACTACGCTCTCGCTGCGTAATCGAAGA
ATAGTAGATTAGACGCTTCATCGCCGCCAAAGTGGCAGCGACGA
GACATCGCCCGAGCAGCTTTTTCCCGAAGTAGCTCGATGGTGCG
20 GTGCTGACAAATCGGGAACCGCTACAGGATGCTTCCTGCCTGTG
GTCAGATCGAACGGAAGATAAGGATCGTGCAATTGGGTCGTTTCA
GCCTCCGCTCGCTCACGAAAATTCCAACCTGAACTAAACATGTA
GAAAGCATATTGATTCCATGTTTGGACGAGGGTTCAATTCCCTCC
AGCTCCACCA SEQ ID NO: 95

Porphyromonas gingivalis tmRNA

GGGGCUGACCGGCUUUGACAGCGUGAUGAAGCGGUAUGUAAG
CAUGUAGUGCGUGGGUGGCUUGCACUAUAAUCUCAGACAUCA
AAAGUUUAAUUGGCGAAAAUAACUACGCUCUCGCUGCGUAAU
5 CGAAGAAUAGUAGAUUAGACGCUUCAUCGCCGCCAAAGUGGCA
GCGACGAGACAUCGCCCCGAGCAGCUUUUUUCCCGAAGUAGCUCG
AUGGUGCGGUGCUGACAAAUCGGGAACCGCUACAGGAUGCUUC
CUGCCUGUGGUCAGAUCGAACGGAAGAUAAAGGAUCGUGCAUU
GGGUCGUUUCAGCCUCCGCUCGCUCACGAAAAUUCCAACUGAA
10 ACUAAACAUGUAGAAAGCAUAUUGAUUCCAUGUUUGGACGAG
GGUUCAAUUCCCUCCAGCUCCACCA SEQ ID NO: 96

Proteus rettgeri ssrA (NCTC 10975), internal partial

GGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGGCGGTTGGCCT
15 CGTAAAAAGCCGCAAAAAAATAGTCGCAAACGACGAAAACCTAC
GCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCTAGCC
TCCGCTCTTGGACGGGGATCAAGAGAGGTCAAACCCAAAAGAG
ATCGCGTGGATGCCTTGCCTGGGGTTGAAGCGTTAACTTAATC
AGGATAGTTTGTGTTGGTGGCGTGTCTGTCCGCAGCTGGCAAATGA
20 ATTCAAAGACTAGACTAAGCATGTAGTACCGAGGATGTAGAAAT
TTC SEQ ID NO: 97

Proteus rettgeri tmRNA (NCTC 10975), internal partial

GGGAUUUGCGAAACCCAAGGUGCAUGCCGAGGGGGCGGUUGGCC
25 UCGUAAAAAGCCGCAAAAAAAUAGUCGCAAACGACGAAAACU

ACGCUUUAGCAGCUUAAUAACCUGCUUAGAGCCCUCUCUCCCU
AGCCUCCGCUCUUGGACGGGGAUCAAGAGAGGUCAAACCCAAA
AGAGAUCGCGUGGAUGCCUUGCCUGGGGUUGAAGCGUUAAC
UUAUUCAGGAUAGUUUGUUGGUGGCGUGUCUGUCCGCAGCUG
5 GCAAUGAAUUCAAAGACUAGACUAAGCAUGUAGUACCGAGG
AUGUAGAAAUUUC SEQ ID NO: 98

Pseudoalteromonas haloplanktoni ssrA, internal partial

GGAATTCAAGAAGCCCGAGGTGCATGTCGAGGTGCGGTTTGCCT
10 CGTAAAAAAGCCGCAATTTAAAGTAATCGCAAACGACGATAACT
ACTCTCTAGCAGCTTAGGCTGGCTAGCGCTCCTTCCATGTATTCT
TGTGGACTGGATTTTGGAGTGTCACCCTAACACCTGATCGCGAC
GGAAACCCTGGCCGGGGTTGAAGCGTTAAACTAAGCGGCCTCG
CCTTTATCTACCGTGTTTGTCCGGGATTTAAAGGTTAATTAAATG
15 ACAATACTAAACATGTAGTACCGACGGTCGAGGCTTTTCGGACG
GGG SEQ ID NO: 99

Pseudoalteromonas haloplanktoni tmRNA, internal partial

GGAAUUCAAGAAGCCCGAGGUGCAUGUCGAGGUGCGGUUUGC
20 CUCGUAAAAAAGCCGCAAUUUAAAGUAAUCGCAAACGACGAU
AACUACUCUCUAGCAGCUUAGGCUGGCUAGCGCUCCUCCAUG
UAUUCUUGUGGACUGGAUUUUGGAGUGUCACCCUAACACCUG
AUCGCGACGGAAACCCUGGCCGGGGUUGAAGCGUUAACUAA
GCGGCCUCGCCUUUAUCUACCGUGUUUGUCCGGGAUUUAAAGG

UUA AUU AAA AUG ACA AU ACU AAA CAU GU AGU ACC GAC GGU CGA
GGC UUU UCG GAC GGGG SEQ ID NO: 100

Pseudomonas aeruginosa ssrA

5 GGGGCCGATTAGGATTCGACGCCGGTAACAAAAGTTGAGGGGC
ATGCCGAGTTGGTAGCAGAACTCGTAAATTCGCTGCTGCAAAC
TATAGTTGCCAACGACGACAACCTACGCTCTAGCTGCTTAATGCG
GCTAGCAGTCGCTAGGGGGATGCCTGTAAACCCGAAACGACTGTC
AGATAGAACAGGATCGCCGCCAAGTTCGCTGTAGACGTAAACGGC
10 TAAAACCTCATACAGCTCGCTCCAAGCACCCCTGCCACTCGGGCGG
CGCGGAGTTAACTCAGTAGAGCTGGCTAAGCATGTAAAACCGAT
AGCGGAAAGCTGGCGGACGGGGGGTTCAAATCCCCCGGTTCCAC
CA SEQ ID NO: 101

15 *Pseudomonas aeruginosa tmRNA*

GGGGCCGAUUAGGAUUCGACGCCGGUAACAAAAGUUGAGGGG
CAUGCCGAGUUGGUAGCAGAACUCGUAAAUUCGCUGCUGCAAA
CUUAUAGUUGCCAACGACGACAACUACGCUCUAGCUGCUUAAU
GCGGCUAGCAGUCGCUAGGGGAUGCCUGUAAACCCGAAACGAC
20 UGUCAGAUAGAACAGGAUCGCCGCCAAGUUCGCUGUAGACGUA
ACGGCUAAAACUCAUACAGCUCGCUCCAAGCACCCUGCCACUC
GGGCGGCGCGGAGUUAACUCAGUAGAGCUGGCUAAGCAUGUA
AAACCGAUAGCGGAAAGCUGGCGGACGGGGGUUCAAUCCCCC
CGGUUCCACCA SEQ ID NO: 102

Salmonella typhimurium ssrA

GGGGCTGATTCTGGATTCGACGGGATTTGCGAAACCCAAGGTGC
ATGCCGAGGGGGCGGTTGGCCTCGTAAAAAGCCGCAAAAAAATA
GTCGCAAACGACGAAACCTACGCTTTAGCAGCTTAATAACCTGC
5 TTAGAGCCCTCTCTCCCTAGCCTCCGCTCTTAGGACGGGGATCAA
GAGAGGTCAAACCCAAAAGAGATCGCGCGGATGCCCTGCCTGG
GGTTGAAGCGTTAAAACGAATCAGGCTAGTCTGGTAGTGGCGTG
TCCGTCCGCAGGTGCCAGGCGAATGTAAAGACTGACTAAGCATG
TAGTACCGAGGATGTAGGAATTTTCGGACGCGGGTTCAACTCCCG
10 CCAGCTCCACCA SEQ ID NO: 103

Salmonella typhimurium tmRNA

GGGGCUGAUUCUGGAUUCGACGGGAUUUGCGAAACCCAAGGU
GCAUGCCGAGGGGGCGGUUGGCCUCGUAAAAAGCCGCAAAAAAA
15 UAGUCGCAAACGACGAAACCUACGCUUUAGCAGCUUAAUAACC
UGC UUAGAGCCCUCUCUCCCUAGCCUCCGCUCUUAGGACGGGG
AUCAAGAGAGGUCAAACCCAAAAGAGAU CGCGCGGAUGCCCUG
CCUGGGGUUGAAGCGUUA AACGAAUCAGGCUAGUCUGGUAG
UGGCGUGUCCGUCCGCAGGUGCCAGGCGAAUGUAAAGACUGAC
20 UAAGCAUGUAGUACCGAGGAUGUAGGAAUUUCGGACGCGGGU
UCAACUCCCGCCAGCUCCACCA SEQ ID NO: 104

Shewanella putrefaciens ssrA

GGGGGCGATTCTGGATTCGACAGGATTCACGAAACCCTGGGAGC
25 ATGCCGAGGGGGCGGTTGGCCTCGTAAAAAGCCGCAAAGTTATAG

TTGCAAACGACGATAACTACGCTCTAGCCGCTTAATGCCGCTAG
CCATCTACCACACGCTTTGCACATGGGCAGTGGATTTGATGGTCA
TCTCACATCGTGCTAGCGAGGGAACCCTGTCTGGGGGTGAACCG
CGAAACAGTACCGGACTCACCGTGTGGGATCCTGTCTTTCGGAG
5 TTCAAACGGTTAAACAATAGAAAGACTAAGCATGTAGCGCCTTG
GATGTAGGTTTTCTGGACGCGGGTTCAAGTCCCGCCGCCTCCACC
A SEQ ID NO: 105

Shewanella putrefaciens tmRNA

10 GGGGGCGAUUCUGGAUUCGACAGGAUUCACGAAACCCUGGGA
GCAUGCCGAGGGGGCGGUUGGCCUCGUAAAAAGCCGCAAAGUUA
UAGUUGCAAACGACGAUAACUACGCUCUAGCCGCUUAAUGCCG
CUAGCCAUCUACCACACGCUUUGCACAUGGGCAGUGGAUUUGA
UGGUCAUCUCACAUCGUGCUAGCGAGGGAACCCUGUCUGGGGG
15 UGAACCGCGAAACAGUACCGGACUCACCGUGUGGGAUCCUGUC
UUUCGGAGUUCAAACGGUUAACAUAAGAAAGACUAAGCAUG
UAGCGCCUUGGAUGUAGGUUUUCUGGACGCGGGUUCAAGUCCC
GCCGCCUCCACCA SEQ ID NO: 106

20 *Staphylococcus aureus* *ssrA*

GGGGACGTTCATGGATTTCGACAGGGGTCCCCCGAGCTCATTAAG
CGTGTCGGAGGGTTGTCTTCGTCATCAACACACACAGTTTATAAT
AACTGGCAAATCAAACAATAATTTTCGCAGTAGCTGCCTAATCGC
ACTCTGCATCGCCTAACAGCATTTTCCTATGTGCTGTTAACGCGAT
25 TCAACCTTAATAGGATATGCTAAACACTGCCGTTTGAAGTCTGTT

TAGAAGAACTTAATCAAACCTAGCATCATGTTGGTTGTTTATCAC
TTTTCATGATGCGAAACCTATCGATAAACTACACACGTAGAAAG
ATGTGTATCAGGACCTTTGGACGCGGGTTCAAATCCCGCCGTCTC
CACCA SEQ ID NO: 107

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Staphylococcus aureus tmRNA

GGGGACGUUCAUGGAUUCGACAGGGGUCCCCCGAGCUCAUUA
GCGUGUCGGAGGGUUGUCUUCGUCAUCAAACACACAGUUUAU
AAUAAACUGGCAAUAACAUAUAUUUCGCAGUAGCUGCCUA
10 AUCGCACUCUGCAUCGCCUAACAGCAUUUCCUAUGUGCUGUUA
ACGCGAUUCAACCUUAAUAGGAUAUGC UAAACACUGCCGUUUG
AAGUCUGUUUAGAAGAAACUUAUAUCAAACUAGCAUCAUGUUG
GUUGUUUAUCACUUUUUCAUGAUGCGAAACCUAUCGAUAAACU
ACACACGUAGAAAGAUGUGUAUCAGGACCUUUGGACGCGGGU
15 UCAAAUCCCGCCGUCUCCACCA SEQ ID NO: 108

Streptococcus gordonii ssrA

GGGGTCGTTACGGATTTCGACAGGCATTATGAGGCATATTTTGCG
ACTCATCTAGCGGATGTAAAACGCCAGTTAAATATAACTGCAAA
20 AAATAATACTTCTTACGCTTTAGCTGCCTAAAAACCAGCGGGCG
TGACCCGATTCGGATTGCTTGTGTCTGATGACAGGTCTTATTATT
AGCAAGCTACGGTAGAATCTTGTCTAGTGATTTTACAAGAGATT
GATAGACTCGCTTGATTTGGGCTTGAGTTATGTGTCAAAATCAAG
TTAAAACAATACATAGCCTATGGTTGTAGACAAATGTGTTGGCA

GATGTTTGGACGTGGGTTCGACTCCCACCGGCTCCACCA SEQ ID
NO: 109

Streptococcus gordonii tmRNA

5 GGGGUCGUUACGGAUUCGACAGGCAUUAUGAGGCAUAUUUUG
CGACUCAUCUAGCGGAUGUAAAACGCCAGUUAAAUAUAACUGC
AAAAAAUAUACUUCUUACGCUUUAGCUGCCUAAAAACCAGCG
GGCGUGACCCGAUUCGGAUUGCUUGUGUCUGAUGACAGGUCU
UAUUUUUAGCAAGCUACGGUAGAAUCUUGUCUAGUGAUUUUA
10 CAAGAGAUUGAUAGACUCGCUUGAUUUUGGGCUUGAGUUAUGU
GUCAAAAUCAAGUUAAAACAAUACAUAAGCCUAUGGUUGUAGA
CAAUGUGUUGGCAGAUUUUGGACGUGGGUUCGACUCCCACC
GGCUCCACCA SEQ ID NO: 110

15 *Streptococcus mutans* ssrA

GGGGTCGTTACGGATTCGACAGGCATTATGAGACCTATTTTGCG
ACTCATCTAGCGGATGTAAAACGCCAGTTAAATATAACTGCAAA
AAATACAAATTCTTACGCAGTAGCTGCCTAAAAACCAGCCTGTG
TGATCAATAACAAATTGCTTGTGTTTGTGATTGGTCTTATTGTTA
20 ACAAGCTACGTTAGAACTGAGTCAGGCTGTTCTAAAAGAGTTCT
ACTGACTCGCATCGTTAGAGTTTGAGTTATGTATTGTAACGGTGT
TAAATAAACACATAACCTATAGTTGTAGACAAATGGGGTTAGCAG
ATGTTTGGACGTGGGTTCGACTCCCACCGGCTCCACCA
SEQ ID NO: 111

Streptococcus mutans tmRNA

GGGGUCGUUACGGAUUCGACAGGCAUUAUGAGACCUAUUUUG
CGACUCAUCUAGCGGAUGUAAAACGCCAGUUAAAUAUAACUGC
AAAAAAUACAAAUUCUUACGCAGUAGCUGCCUAAAAACCAGCC
5 UGUGUGAUCAAUAACAAAUUGCUUGUGUUUGUUGAUUGGUCU
UAUUGUUAACAAGCUACGUUAGAACUGAGUCAGGCUGUUCUA
AAAGAGUUCUACUGACUCGCAUCGUUAGAGUUUGAGUUAUGU
AUUGUAAACGGUGUUAAAUAACACAUAACCUAUAGUUGUAGA
CAA AUGGGUUAGCAGAUGUUUGGACGUGGGGUUCGACUCCCACC
10 GGCUCCACCA SEQ ID NO: 112

Streptococcus pneumoniae ssrA

GGGGTCGTTACGGATTCGACAGGCATTATGAGGCATATTTTGCG
ACTCGTGTGGCGACGTAAACGCTCAGTTAAATATAACTGCAAAA
15 AATAACACTTCTTACGCTCTAGCTGCCTAAAAACCAGCAGGCGT
GACCCGATTTGGATTGCTCGTGTTCAATGACAGGTCTTATTATTA
GCGAGATACGATTAAGCCTTGTCTAGCGGTTTGATAAGAGATTG
ATAGACTCGCAGTTTCTAGACTTGAGTTATGTGTCGAGGGGGCTGT
TAAAATAATACATAACCTATGGTTGTAGACAAATATGTTGGCAG
20 GTGTTTGGACGTGGGTTCGACTCCCACCGGCTCCACCA
SEQ ID NO: 113

Streptococcus pneumoniae tmRNA

GGGGUCGUUACGGAUUCGACAGGCAUUAUGAGGCAUAUUUUG
25 CGACUCGUGUGGCGACGUAAACGCUCAGUUAAAUAUAACUGCA

AAAAUAACACUUCUUACGCUCUAGCUGCCUAAAAACCAGCAG
GCGUGACCCGAUUUGGAUUGCUCGUGUUCUAAUGACAGGUCUU
AUUAUUAGCGAGAUACGAUUAAGCCUUGUCUAGCGGUUUGAU
AAGAGAUUGAUAGACUCGCAGUUUCUAGACUUGAGUUAUGUG
5 UCGAGGGGCUGUUAAAAUAAUACAUAACCUAUGGUUGUAGAC
AAAU AUGUUGGCAGGUGUUUGGACGUGGGUUCGACUCCCACC
GGCUCCACCA SEQ ID NO: 114

Streptococcus pyogenes ssrA

10 GGGGTTGTTACGGATTTCGACAGGCATTATGAGGCATGTTTTGCGT
CCCATCGGCAGATGTAAATTGCCAGTTAAATATAACTGCAAAAA
ATACAAACTCTTACGCTTTAGCTGCCTAAAAACCAGCTAGCGTG
ACTTCTACAAGATTGCTTGTGTCCTGTTAGAAGTCTCAAAATAGC
AAGCTACGGTTACGAAATTGTCTAGTTTCGTGACAAGAGATTGA
15 TAGACTCGCAAATAATGGCTTGAGTTATGTGTCTTTAGTTTGTT
AAATGAAGACATAACCTATGGACGTAGACAAATATGTTGGCAGG
TGTTTGGACGTGGGTTCGACTCCCACCAGCTCCACCA
SEQ ID NO: 115

20 *Streptococcus pyogenes tmRNA*

GGGGUUGUUACGGAUUCGACAGGCAUUAUGAGGCAUGUUUUG
CGUCCCAUCGGCAGAUUGUAAAUUGCCAGUUAAAUAUAACUGCA
AAAAAUACAAACUCUUACGCUUUAGCUGCCUAAAAACCAGCUA
GCGUGACUUCUACAAGAUUGCUGUGUCCUGUUAGAAGUCUC
25 AAAAUAGCAAGCUACGGUUACGAAAUUGUCUAGUUUCGUGAC

AAGAGAUUGAUAGACUCGCAAACUAAUGGCUUGAGUUAUGUG
UCUUUAGUUUGUUA AAAUGAAGACAUAACCUAUGGACGUAGAC
AAAU AUGUUGGCAGGUGUUUGGACGUGGGUUCGACUCCCACC
AGCUCCACCA SEQ ID NO: 116

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Synechococcus sp. PCC6301 *ssrA*

GGGGCTGTAATGGTTTCGACGTGTTGGTGAATCCTTCACCGTGAT
TCAGGCCGAGAGGGAGTCCACTCTCGTAAATCCAGGCTCAACCA
AAAGTAACTGCGAACAACATCGTTCCTTTCGCTCGTAAAGGCTGCTCC
10 TGTAGCTGCTTAAACGCCACAACTTTCTGGCTCGAGCGTCTAGTCG
TAGACTCCGTTAATACGCCTAGACTTAAACCCCCAACGGATGCT
CGAGTGGCGGCCTCAGGTCCGTCCTCTCGCTAAGCAAAAACCTG
AGCATCCCGCCAACGGGGATAATCGTTGGCTCCCGCACAGTGGG
TCAACCGTGCTAAGCCTGTGAACGAGCGGAAAGTTACTAGTCAA
15 TGCGGACAGCGGTTCGATTCCGCTCAGCTCCACCA
SEQ ID NO: 117

Synechococcus sp. PCC6301 tmRNA

GGGGCUGUAAUGGUUUCGACGUGUUGGUGAAUCCUUCACCGU
20 GAUUCAGGCCGAGAGGGAGUCCACUCUCGUAAAUCCAGGCUCA
ACCAAAAGUAAACUGCGAACAACAUCGUUCCUUUCGCUCGUAAAG
GCUGCUCCUGUAGCUGCUUAAACGCCACAAACUUUCUGGCUCG
AGCGUCUAGUCGUAGACUCCGUUAAUACGCCUAGACUUA AACC
CCCAACGGAUGCUCGAGUGGCGGCCUCAGGUCCGUCCUCUCGC
25 UAAGCAAAAACCUGAGCAUCCCGCCAACGGGGAUAAUCGUUGG

CUCCCGCACAGUGGGUCAACCGUGCUAAGCCUGUGAACGAGCG
GAAAGUUACUAGUCA AUGCGGACAGCGGUUCGAU UCCGCUCAG
CUCCACCA SEQ ID NO: 118

5 *Synechocystis* sp. PCC6803 *ssrA*

GGGGCCGCAATGGTTTCGACAGGTTGGCGAAAGCTTGCCCCGTGA
TACAGGTCGAGAGTGAGTCTCCTCTCGCAAATCAAAGGCTCAAA
AAAAAGTAACTGCGAATAACATCGTCAGCTTCAAACGGGTAGCC
ATAGCAGCCTAGTCTGTAAAAGCTACATTTTCTTGTCAAAGACCG
10 TTTACTTCTTTTCTGACTCCGTTAAGGATTAGAGGTTAACCCCAA
CGGATGCTTTGTTTGGCTCTTCTCTAGTTAGCTAAACAATCAAGA
CTCAGACTAGAGCATCCCACCATCAGGGATAATCGATGGTCCCC
GTCCTAGGGCTAGAAGGACTAAACCTGTGAATGAGCGGAAAGTT
AATACCCAGTTTGGACAGCAGTTCAATTCTGCTCGGCTCCACCA
15 SEQ ID NO: 119

Synechocystis sp. PCC6803 tmRNA

GGGGCCGCAAUGGUUUCGACAGGUUGGCGAAAGCUUGCCCGUG
AUACAGGUCGAGAGUGAGUCUCCUCUCGCAAAUCAAGGCUCA
20 AAAAAAAGUAAACUGCGAAUAACAUCGUCAGCUUCAACGGGU
AGCCAUAGCAGCCUAGUCUGUAAAAGCUACA UUUUCUUGUCA
AGACCGUUUACUUCUUUUCUGACUCCGUUAAGGAUUAGAGGU
UAACCCCAACGGAUGCUUUGUUUGGCUCUUCUCUAGUUAGCUA
AACAAUCAAGACUCAGACUAGAGCAUCCCACCAUCAGGGGAUAA
25 UCGAUGGUCCCCGUCCUAGGGGCUAGAAGGACUAAACCUGUGAA

UGAGCGGAAAGUUAAUACCCAGUUUGGACAGCAGUUCAAUUC
UGCUCGGCUCCACCA SEQ ID NO: 120

Thermotoga maritima ssrA

5 GGGGGCGAACGGGTTCGACGGGGATGGAGTCCCCTGGGAAGCG
AGCCGAGGTCCCCACCTCCTCGTAAAAAAGGTGGGACAAAGAAT
AAGTGCCAACGAACCTGTTGCTGTTGCCGCTTAATAGATAAGCG
GCCGTCCTCTCCGAAGTTGGCTGGGCTTCGGAAGAGGGGCGTGAG
AGATCCAGCCTACCGATTCAGCTTCGCCTTCCGGCCTGAATCGGG
10 AAAACTCAGGAAGGCTGTGGGAGAGGACACCCTGCCCCGTGGGA
GGTCCCTCCCGAGAGCGAAAACACGGGCTGCGCTCGGAGAAGCC
CAGGGGCCTCCATCTTCGGACGGGGGTTCGAATCCCCCCGCCTC
CACCA SEQ ID NO: 121

15 *Thermotoga maritima tmRNA*

GGGGGCGAACGGGUUCGACGGGGAUGGAGUCCCCUGGGAAGC
GAGCCGAGGUCCCCACCUCCUCGUAAAAAAGGUGGGACAAAGA
AUAAGUGCCAACGAACCUGUUGCUGUUGCCGCUUAAUAGAU
AGCGGCCGUCUCCGAAGUUGGCUGGGCUUCGGAAGAGGGC
20 GUGAGAGAUCCAGCCUACCGAUUCAGCUUCGCCUUCGCGCCUG
AAUCGGGAAAACUCAGGAAGGCUGUGGGAGAGGACACCCUGCC
CGUGGGAGGUCCCUCCCGAGAGCGAAAACACGGGCUGCGCUCG
GAGAAGCCCAGGGGCCUCCAUCUUCGGACGGGGGUUCGAAUCC
CCCCGCCUCCACCA SEQ ID NO: 122

Thermus thermophilus ssrA

GGGGGTGAAACGGTCTCGACGGGGGTCGCCGAGGGGCGTGGCTG
CGCGCCGAGGTGCGGGTGGCCTCGTAAAAACCCGCAACGGCATA
ACTGCCAACACCAACTACGCTCTCGCGGCTTAATGACCGCGACC
5 TCGCCCCGGTAGCCCTGCCGGGGGGCTCACCGGAAGCGGGGACACA
AACCCGGCTAGCCCGGGGGCCACGCCCTCTAACCCCGGGCGAAGC
TTGAAGGGGGGCTCGCTCCTGGCCGCCCCGTCCGCGGGGCAAGCCA
GGAGGACACGCGAAACGCGGACTACGCGCGTAGAGGCCCGCCG
TAGAGACCTTCGGACGGGGGGTTCGACTCCCCCCACCTCCACCA
10 SEQ ID NO: 123

Thermus thermophilus tmRNA

GGGGGUGAAACGGUCUCGACGGGGGUCGCCGAGGGGCGUGGCU
GCGCGCCGAGGUGCGGGUGGCCUCGUAAAAACCCGCAACGGCA
15 UAACUGCCAACACCAACUACGCUCUCGCGGCUUAAUGACCGCG
ACCUCGCCCCGGUAGCCCUGCCGGGGGGCUCACCGGAAGCGGGGA
CACAAACCCGGCUAGCCCCGGGGGCCACGCCUCUAACCCCGGGC
GAAGCUUGAAGGGGGGCUCGCUCCUGGCCGCCCCGUCCGCGGGCC
AAGCCAGGAGGACACGCGAAACGCGGACUACGCGCGUAGAGGC
20 CCGCCGUAGAGACCUUCGGACGGGGGUUCGACUCCCCCCACCU
CCACCA SEQ ID NO: 124

Treponema pallidum ssrA

GGGGATGACTAGGTTTCGACTAGGGATGTGGGGTGTTGCGCTGC
25 AGGTGGAGTGTCGATCTCCTGATTCGGCGCCTTTATAACTGCCAA

TTCTGACAGTTTCGACTACGCGCTCGCCGCGTAATCGCGGGGCCTG
TGTTTGCGCTGCTCTGAGCGAACATATCGGCCCCGACGCCAAACG
GAGCTTGCTCTTACGTTGTGCACGGCGGACGTAGGGGGGACTTTT
GTCTGTGCTAAGACTCTGGCGCGTGCGGTGCAGGCCTAGCAGAG
5 TCCGACAAACGCAGTACGCACCGCTAAACCTGTAGGCGCGCAGC
ACTCGCTCTTTAGGACGGGGGGTTCGATTCCCCCCATCTCCACCA
SEQ ID NO: 125

Treponema pallidum tmRNA

10 GGGGAUGACUAGGUUUCGACUAGGGAUGUGGGGUGUUGCGCU
GCAGGUGGAGUGUCGAUCUCCUGAUUCGGCGCCUUUAUAACUG
CCAAUUCUGACAGUUUCGACUACGCGCUCGCCGCGUAAUCGCG
GGCCUGUGUUUGCGCUGCUCUGAGCGAACAUUUCGGCCCCGACG
CCAAACGGAGCUUGCUCUUACGUUGUGCACGGCGGACGUAGGG
15 GGACUUUUGUCUGUGCUAAGACUCUGGGCGCGUGCGGUGCAGGC
CUAGCAGAGUCCGACAAACGCAGUACGCACCGCUAAACCUGUA
GGCGCGCAGCACUCGCUCUUUAGGACGGGGGUUCGAUUCCCCC
CAUCUCCACCA SEQ ID NO: 126

20 *Vibrio cholerae* ssrA

GGGGCTGATTCAGGATTCGACGGGAATTTTGCAGTCTGAGGTGC
ATGCCGAGGTGCGGTAGGCCTCGTTAACAAACCGCAAAAAAATA
GTCGCAAACGACGAAAACACTACGCACTAGCAGCTTAATACCCTGC
TCAGAGCCCTTCCTCCCTAGCTTCCGCTTGTAAGACGGGGGAAATC
25 AGGAAGGTCAAACCAAATCAAGCTGGCGTGGATTCCCCCACCTG

AGGGATGAAGCGCGAGATCTAATTCAGGTTAGCCATTCGTTAGC
GTGTCGGTTCGCAGGCGGTGGTGAAATTAAAGATCGACTAAGCA
TGTAGTACCAAAGATGAATGGTTTTTCGGACGGGGGGTTCAACTCC
CCCCAGCTCCACCA SEQ ID NO: 127

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Vibrio cholerae tmRNA

GGGGCUGAUUCAGGAUUCGACGGGAAUUUUGCAGUCUGAGGU
GCAUGCCGAGGUGCGGUAGGCCUCGUUAACAAACCGCAAAAAA
AUAGUCGCAAACGACGAAAACUACGCACUAGCAGCUUAAUACC
10 CUGCUCAGAGCCCUUCCUCCCUAGCUUCCGCUUGUAAGACGGG
GAAAUCAGGAAGGUCAAACCAAAUCAAGCUGGCGUGGAUUCCC
CCACCUGAGGGAUGAAGCGCGAGAUCAAUUCAGGUUAGCCAU
UCGUUAGCGUGUCGGUUCGCAGGCGGUGGUGAAAUUAAGAU
CGACUAAGCAUGUAGUACCAAAGAUGAAUGGUUUUCGGACGG
15 GGGUUCAACUCCCCCCAGCUCCACCA SEQ ID NO: 128

Yersinia pestis *ssrA*

GGGGCTGATTCTGGATTCGACGGGATTCGCGAAACCCAAGGTGC
ATGCCGAGGTGCGGTGGCCTCGTAAAAAACCGCAAAAAAAATA
20 GTTGCAAACGACGAAAACCTACGCACTAGCAGCTTAATAACCTGC
TTAGAGCCCTCTCTGCCTAGCCTCCGCTCTTAGGACGGGGATCAA
GAGAGGTCAAACCTAAAAGAGCTCGTGTGGAAACCTTGCCTGGG
GTGGAAGCATTAAACTAATCAGGATAGTTTGTGAGTAGCGTGT
CCATCCGCAGCTGGCCGGCGAATGTAATGATTGGACTAAGCATG

TAGTGCCGACGGTGTAGTAATTTTCGGACGGGGGTTCAAATCCCC
CCAGCTCCACCA SEQ ID NO: 129

Yersinia pestis tmRNA

5 GGGGCUGAUUCUGGAUUCGACGGGAUUCGCGAAACCCAAGGU
GCAUGCCGAGGUGCGGUGGCCUCGUAAAAAACCGCAAAAAAAAAA
UAGUUGCAAACGACGAAAACUACGCACUAGCAGCUUAAUAACC
UGCUUAGAGCCCUCUCUGCCUAGCCUCCGCUCUUAGGACGGGG
AUCAAGAGAGGUCAAACCUAAAAGAGCUCGUGUGGAAACCUU
10 GCCUGGGGUGGAAGCAUUA AACUAAUCAGGAUAGUUUGUCA
GUAGCGUGUCCAUCCGCAGCUGGCCGGCGAAUGUAAUGAUUGG
ACUAAGCAUGUAGUGCCGACGGUGUAGUAAUUUCGGACGGGG
GUUCAAAUCCCCCCCAGCUCCACCA SEQ ID NO: 130

15 *Campylobacter fetus* *ssrA*, internal partial

AGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGGCAAAGCGT
AAAAAGCCCAAATAAAATTAAACGCAAACAACGTTAAATTCGCT
CCTGCTTACGCTAAAGCTGCGTAAGTTCAGTTGAGCCTGAAATTT
AAGTCATACTATCTAGCTTAATTTTCGGTCATCTTTGATAGTGTA
20 GCCTTGCGTTTGACAAGCGTTGAGGTGAAATAAAGTCTTAGCCTT
GCTTTTGAGTTTTTGGAAGATGAGCGAAGTAGGGTGAAGTAGTCA
TCTTTGCTAAGCATGTAGAGGTCTTTGTGGGATTATTTTGG
SEQ ID NO: 131

Campylobacter fetus tmRNA, internal partial

AGGAGUAAGUCUGCUUAGAUGGCAUGUCGCUUUGGGCAAAGC
GUAAAAAGCCCCAAAUAAAAUUAACGCAAACAACGUUAAAAU
CGCUCCUGCUUACGCUAAAGCUGCGUAAGUUCAGUUGAGCCUG
5 AAAUUUAAGUCAUACUAUCUAGCUUAAUUUUCGGUCAUCUUU
GAUAGUGUAGCCUUGCGUUUGACAAGCGUUGAGGUGAAAUA
AGUCUUAGCCUUGCUUUUGAGUUUUGGAAGAUGAGCGAAGUA
GGGUGAAGUAGUCAUCUUUGCUAAGCAUGUAGAGGUCUUUGU
GGGAUUUUUUUGG SEQ ID NO: 132

10

Campylobacter coli (BM2509) *ssrA*, internal partial

AGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGACAAAGCGT
AAAAAGTCCAAATTAATAAATTAACGCAAATAACGTAAATTTGC
TCCTGCTTACGCTAAAGCTGCGTAAGTTCAGTTGAGCCCGAAACT
15 CAAGTGATGCTATCTAGCTTGAATTTTGGTCATCTTTGATAGTGT
AGATTGAAAATTGACAACCTTTTAATCGAAGTTAAAGTCTTAGTCT
AGCTTGAAATTTTGGGAAGGTGAGTTTAGCCAGATGAAGTTTTCA
CCTTTGCTAAACATGTAGAAGTCTTTGTGGGGTTATTTTTGG
SEQ ID NO: 133

20

Campylobacter coli (BM2509) tmRNA, internal partial

AGGAGUAAGUCUGCUUAGAUGGCAUGUCGCUUUGGACAAAGC
GUAAAAAGUCCAAAUAAAAUUAACGCAAUAACGUUAAAU
UUGCUCUGCUUACGCUAAAGCUGCGUAAGUUCAGUUGAGCCC
25 GAAACUCAAGUGAUGCUAUCUAGCUUGAAUUUUGGUCAUCUU

UGAUAGUGUAGAUUGAAAAUUGACAACUUUUAUCGAAGUUA
AAGUCUUAGUCUAGCUUGAAAUUUUGGAAGGUGAGUUUAGCC
AGAUGAAGUUUUCACCUUUGCUAAACAUGUAGAAGUCUUUGU
GGGGUUAUUUUUGG SEQ ID NO: 134

5

Camplyobacter chicken isolate *ssrA*, internal partial

ACAGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGGCAAAGC
GTAAAAAGCCCAAATAAAATTAAACGCAAACAACGTAAATTTCG
CTCCTGCTTACGCTAAAGCTGCGTAAGTTCAGTTGAGCCTGAAAT
10 TTAAGTCATACTATCTAGCTTAATTTTCGGTCATTTTTTGATAGTGT
AGCCTTGCGTTTGACAAGCGTTGAGGTGAAATAAGGTCTTAGCC
TTGCTTTTGAGTTTTGGAAGATGAGCGAAGTAGGGTGAAGTAGT
CATCTTTGCTAAGCATGTAGAGGTCTTTGTGGGATTATTTTTGG
SEQ ID NO: 135

15

Camplyobacter chicken isolate tmRNA, internal partial

ACAGGAGUAAGUCUGCUUAGAUGGCAUGUCGCUUUGGGCAA
GCGUAAAAAGCCCAAUAAAAUUAAACGCAAACAACGUUAAA
UUCGCUCCUGCUUACGCUAAAGCUGCGUAAGUUCAGUUGAGCC
20 UGAAAUUUUAAGUCAUACUAUCUAGCUUAAUUUUUCGGUCAUUU
UUGAUAGUGUAGCCUUGCGUUUGACAAGCGUUGAGGUGAAAU
AAGGUCUUAGCCUUGCUUUUGAGUUUUUGGAAGAUGAGCGAAG
UAGGGUGAAGUAGUCAUCUUUGCUAAGCAUGUAGAGGUCUUU
GUGGGAUUAUUUUUGG SEQ ID NO: 136

25

Clostridium perfringens *ssrA*, internal partial

ACGGGGGTAGGATGGGTTTGATAAGCGAGTCGAGGGAAGCATG
GTGCCTCGATAATAAAGTATGCATTAAAGATAAACGCACGAGAT
AATTTTGCATTAGCAGCTTAAGTTAGCGCTGCTCATCCTTCCTCA
5 ATTGCCCACGGTTGAGAGTAAGGGTGTCAATTTAAAAGTGGGGAA
CCGAGCCTAGCAAAGCTTTGAGCTAGGAACGGAATTTATGAAGC
TTACCAAAGAGGAAGTTTGTCTGTGGACGTTCTCTGAGGGAATTT
TAAACACAAGACTACACTCGTAGAAAGTCTTACTGGTCTGCTTT
CGG SEQ ID NO: 137

10

Clostridium perfringens tmRNA, internal partial

ACGGGGGUAGGAUGGGUUUGAUAAGCGAGUCGAGGGAAGCAU
GGUGCCUCGAUAAUAAAGUAUGCAUUAAGAUAACGCACGA
GAUAAUUUUGCAUUAGCAGCUUAAGUUAGCGCUGCUCAUCCU
15 UCCUCAAUUGCCCACGGUUGAGAGUAAGGGUGUCAUUUAAAA
GUGGGGAACCGAGCCUAGCAAAGCUUUGAGCUAGGAACGGAA
UUUAUGAAGCUUACCAAAGAGGAAGUUUGUCUGUGGACGUUC
UCUGAGGGAAUUUUAAAACACAAGACUACACUCGUAGAAAGU
CUUACUGGUCUGCUUUCGG SEQ ID NO: 138

20

Haemophilus ducreyi (NCTC 10945) *ssrA*, internal partial

ACGGGATTAGCGAAGTCCAAGGTGCACGTCGAGGTGCGGTAGGC
CTCGTAACAAACCGCAAAAAAATAGTCGCAAACGACGAACAAT
ACGCTTTAGCAGCTTAATAACCTGCATTTAGCCTTCGCGCCCTAG
25 CTTTCGCTCGTAAGACGGGGAGCACGCGGAGTCAAACCAAAACG

AGATCGTGTGGACGCTTCCGCTTGTAGATGAAACACTAAATTGA
ATCAAGCTAGTTTATTTCTTGCGTGTCTGTCCGCTGGAGATAAGC
GAAATTAAAGACCAGACTAAACGTGTAGTACTGAAGATAGAGTA
ATTTTCGGACCCGGGTTCGACTC SEQ ID NO: 139

5

Haemophilus ducreyi (NCTC 10945) tmRNA, internal partial

ACGGGAUUAGCGAAGUCCAAGGUGCACGUCGAGGUGCGGUAG
GCCUCGUAACAAACCGCAAAAAAAAAAUAGUCGAAACGACGAACA
AUACGCUUUAGCAGCUUAAUAACCUGCAUUUAGCCUUCGCGCC
10 CUAGCUUUCGCUUCGUAAGACGGGGAGCACGCGGAGUCAAACCA
AAACGAGAUCGUGUGGACGCUUCCGCUUGUAGAUGAAACACU
AAAUUGAAUCAAGCUAGUUUAUUUCUUGCGUGUCUGUCCGCU
GGAGAUAAAGCGAAAUUAAAGACCAGACUAAACGUGUAGUACU
GAAGAUAGAGUAAUUUCGGACCCGGGUUCGACUC
15 SEQ ID NO: 140

Listeria innocua (food isolate #1) *ssrA*, internal partial

GGCAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAACCAGT
AGCATAGCTGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGG
20 GTCTCACTCTAAGTGGGCTACACTAGTTAATCTCCGTCTGAGGTT
AAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCTGTTAC
CGGGCTGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCG
TAGATATTCAA SEQ ID NO: 141

Listeria innocua (food isolate #1) tmRNA, internal partial

GGCAAAGAAAAACAAAACCUAGCUUUCGCUGCCUAAUAACCAG
UAGCAUAGCUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAA
GGGUCUCACUCUAAGUGGGCUACACUAGUUAAUCUCCGUCUGA
5 GGUUAAAUAAGAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCC
UGUUACCGGGCUGAUGUUUAUGCGAAAUGCUAAUACGGUGAC
UACGCUCGUAGAUUUCAA SEQ ID NO: 142

Listeria innocua (food isolate #2) *ssrA*, internal partial

10 GGCAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGT
AGCATAGCTGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGG
GTCTCACTCTAAGTGGGCTACACTAGTTAATCTCCGTCTGAGGTT
AAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCTGTTAC
CGGGCCGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCG
15 TAGATATTAA SEQ ID NO: 143

Listeria innocua (food isolate #2) tmRNA, internal partial

GGCAAAGAAAAACAAAACCUAGCUUUCGCUGCCUAAUAAGCAG
UAGCAUAGCUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAA
20 GGGUCUCACUCUAAGUGGGCUACACUAGUUAAUCUCCGUCUGA
GGUUAAAUAAGAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCC
UGUUACCGGGCCGAUGUUUAUGCGAAAUGCUAAUACGGUGAC
UACGCUCGUAGAUUUUAA SEQ ID NO: 144

Listeria innocua (food isolate #3) *ssrA*, internal partial

GGCAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGT
AGAATAGCTGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGG
GTCTCACTCTAAGTGGGCTACACTAGTTAATCTCCGTCTGAGGTT
5 AAATAGAAGAGCTTAATCGGACTAGCTGAATGGAAGCCTGTTAC
CGGGCCGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCG
TAGATATTAA SEQ ID NO: 145

Listeria innocua (food isolate #3) tmRNA, internal partial

10 GGCAAAGAAAAACAAAACCUAGCUUUCGCUGCCUAAUAAGCAG
UAGAAUAGCUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAA
GGGUCUCACUCUAAGUGGGCUACACUAGUUAUAUCUCCGUCUGA
GGUUAUAUAGAAGAGCUUAAUCGGACUAGCUGAAUGGAAGCC
UGUUACCGGGCCGAUGUUUAUGCGAAAUGCUAAUACGGUGAC
15 UACGCUCGUAGAUUUUAA SEQ ID NO: 146

Listeria innocua (ATCC 12210) *ssrA*, internal partial

GGCAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGT
AGCATAGCTGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGG
20 GTCTCACTCTAAGTGGGCTACACTAGTTAATCTCCGTCTGGGGTT
AAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCTGTTAC
TGGGCCGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCG
TAGATATTAA SEQ ID NO: 147

Listeria innocua (ATCC 12210) tmRNA, internal partial

GGCAAAGAAAAACAAAACCUAGCUUUCGCUGCCUAAUAAGCAG
UAGCAUAGCUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAA
GGGUCUCACUCUAAGUGGGGCUACACUAGUUAUCUCCGUCUGG
5 GGUUAAAUAAGAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCC
UGUUACUGGGCCGAUGUUUAUGCGAAAUGC UAAUACGGUGAC
UACGCUCGUAGAUUUUAA SEQ ID NO: 148

Listeria ivanovii (NCTC 11846) *ssrA*, internal partial

10 ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGGATCGTCC
TCGTTATTAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA
AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTTTAAGTGG
GCTACACTAAATAATCTCCGTCTGGGGTTAGTTAGAAGAGCTTA
15 ATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTAT
GCGAAATGCTAATAACGGTGACTACGCTCGTAGATATTTAAGTGC
CGATATTTCTGG SEQ ID NO: 149

Listeria ivanovii (NCTC 11846) tmRNA, internal partial

20 ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGGAUCGU
CCUCGUUAUUAACGUCAAAGCCAUAUAUACUGGCAAAGAAA
AACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCU
GAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACU
UUAAGUGGGGCUACACUAAAUAUUCUCCGUCUGGGGUUAGUUA
25 GAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGG

GCUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUCGCUCGUA
GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 150

Listeria seeligeri (NCTC 11856) *ssrA*, internal partial

5 ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGGATCGTCC
TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA
AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
CCGTGCATCGCCCATGTGCTACGGAAAGGGTCTCACTTTAAGTG
GGCTACACTAAATAATCTCCGTCTGGGGTTAGTTAGAAGAGCTT
10 AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA
TGCGAAATACTAATACGGTGACTACGCTCGTAGATATTTAAGTG
CCCATATTTCTGG SEQ ID NO: 151

Listeria seeligeri (NCTC 11856) tmRNA, internal partial

15 ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGGAUCGU
CCUCGUUAUCAACGUCAAAGCCAAUAAUAAACUGGCAAAGAAAA
ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG
AUCCUCCGUGCAUCGCCCAUGUGCUACGGAAAGGGUCUCACUU
UAAGUGGGGCUACACUAAAUAUAUCUCCGUCUGGGGGUUAGUUAG
20 AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG
CUGAUGUUUAUGCGAAAUACUAAUACGGUGACUACGCUCGUA
GAUAUUUAAGUGCCCAUAUUUCUGG SEQ ID NO: 152

Salmonella enteritidis *ssrA*, internal partial

ACGGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGGCGGTTGGC
CTCGTAAAAAGCCGCAAAAAAATAGTCGCAAACGACGAAACCT
ACGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCTAG
5 CCTCCGCTCTTAGGACGGGGATCAAGAGAGGTCAAACCCAAAAG
AGATCGCGTGGATGCCCTGCCTGGGGTTGAAGCGTTAAACGAA
TCAGGCTAGTCTGGTAGTGGCGTGTCCGTCCGCAGGTGCCAGGC
GAATGTAAAGACTGACTAAGCATGTAGTACCGAGGATGTAGGAA
TTTCGG SEQ ID NO: 153

10

Salmonella enteritidis tmRNA, internal partial

ACGGGAUUUGCGAAACCCAAGGUGCAUGCCGAGGGGGCGGUUG
GCCUCGUAAAAAGCCGCAAAAAAAUAGUCGCAAACGACGAAAC
CUACGCUUUAGCAGCUUAAUAACCUGCUUAGAGCCCUCUCUCC
15 CUAGCCUCCGCUCUUAGGACGGGGGAUCAAGAGAGGUCAAACCC
AAAAGAGAU CGCGUGGAUGCCCUGCCUGGGGUUGAAGCGUUA
AAACGAAUCAGGCUAGUCUGGUAGUGGCGUGUCCGUCCGCAGG
UGCCAGGCGAAUGUAAAGACUGACUAAGCAUGUAGUACCGAG
GAUGUAGGAAUUUCGG SEQ ID NO: 154

20

Staphylococcus epidermidis (NCTC 11047) *ssrA*, internal partial

ACAGGGGTCCCCCGAGCTTATTAAGCGTGTCTGGAGGGTTGGCTC
CGTCATCAACACATTTCGGTTAAATATAACTGACAAATCAAACA
ATAATTTTCGCAGTAGCTGCGTAATAGCCACTGCATCGCCTAACA
25 GCATCTCCTACGTGCTGTTAACGCGATTCAACCCTAGTAGGATAT

GCTAAACACTGCCGCTTGAAGTCTGTTTAGATGAAATATAATCA
AGCTAGTATCATGTTGGTTGTTTATTGCTTAGCATGATGCGAAAA
TTATCAATAAACTACACACGTAGAAAGATTTGTATCAGGACCTC
TGG SEQ ID NO: 155

5

Staphylococcus epidermidis (NCTC 11047) tmRNA, internal partial

ACAGGGGUCCCCCGAGCUUAUUAAGCGUGUCGGAGGGUUGGCU
CCGUCAUCAACACAUUUCGGUUAUUAUUAACUGACAAAUCAAA
CAAUAAUUUCGCAGUAGCUGCGUAAUAGCCACUGCAUCGCCUA
10 ACAGCAUCUCCUACGUGCUGUUAACGCGAUUCAACCCUAGUAG
GAUAUGC UAAACACUGCCGCUUGAAGUCUGUUUAGAUGAAAU
AUAAUCAAGCUAGUAUCAUGUUGGUUGUUUAUUGCUUAGCAU
GAUGCGAAAAUUAUCAAUAAACUACACACGUAGAAAGAUUUG
UAUCAGGACCUCUGG SEQ ID NO: 156

15

Streptococcus agalactiae (NCTC 8181) *ssrA*, internal partial

ACAGGCATTATGAGGTATATTTTGCGACTCATCGGCAGATGTAA
AATGCCAGTTAAATATAACTGCAAAAAATACAAATTCTTACGCA
TTAGCTGCCTAAAAAACAGCCTGCGTGATCTTCACAAGATTGTTT
20 GCGTTTTGCTAGAAGGTCTTATTTATCAGCAAACACTACGTTTGGCT
ACTGTCTAGTTAGTTAAAAAGAGATTTATAGACTCGCTATGTGA
GGGCTTGAGTTATGTGTCATCACCTAGTTAAATCAATACATAACC
TATAGTTGTAGACAAATATATTAGCAGATGTTTGG
SEQ ID NO: 157

25

Streptococcus agalactiae (NCTC 8181) tmRNA, internal partial

ACAGGCAUUAUGAGGUUAUUAUUUGCGACUCAUCGGCAGAUGU
AAAAUGCCAGUUAUUAUUAACUGCAAAAAAUACAAAUUCUUA
CGCAUUAGCUGCCUAAAAAACAGCCUGCGUGAUCUUCACAAGA
5 UUGUUUGCGUUUUGCUAGAAGGUCUUAUUUAUCAGCAAACUA
CGUUUGGCUACUGUCUAGUUAGUUAAAAAGAGAUUUUAUAGAC
UCGCUAUGUGAGGGGCUUGAGUUAUGUGUCAUCACCUAGUUAA
AUCAAUACAUAACCUAUAGUUGUAGACAAAUUAUUAGCAGA
UGUUUGG SEQ ID NO: 158

10

Bordetella bronchiseptica *ssrA*

GGGGCCGATCCGGATTTCGACGTGGGTCATGAAACAGCTCAAGGC
ATGCCGAGCACCAGTAAGCTCGTTAATCCACTGGAACACTACAA
ACGCCAACGACGAGCGTTTCGCTCTCGCCGCTTAAGCGGTGAGC
15 CGCTGCACTGATCTGTCCTTGGGTCACGCGGGGGGAA
SEQ ID NO: 159

Bordetella bronchiseptica tmRNA

GGGGCCGAUCCGGAUUCGACGUGGGUCAUGAAACAGCUCAAGGC
20 AUGCCGAGCACCAGUAAGCUCGUUAAUCCACUGGAACACUACAA
ACGCCAACGACGAGCGUUUCGCUCUCGCCGCUUAAGCGGUGAGC
CGCUGCACUGAUCUGUCCUUGGGUCACGCGGGGGGAA
SEQ ID NO: 160

25

Chlamydia pneumoniae (CWL029), *ssrA*

GGGGGTGTATAGGTTTCGACTTGAAAATGAAGTGTTAATTGCAT
GCGGAGGGCGTTGGCTGGCCTCCTAAAAAGCCAACAAAACAATA
AATGCCGAACCTAAGGCTGAATGCGAAATTATTAGCTTGTTTGA
5 CTCAGTAGAGGAAAGACTAGCTGCTTAATTAGCAAAAGTTGTTA
GCTAGATAATCTCTAGGTAACCCGGTATCTGCGAGCTCCACCAG
AGGCTTGCAAAATACCGTCATTTATCTGGTTGGAACCTTACTTTCT
CTAATTCTCAAGGAAGTTCGTTTCGAGATTTTTTGAGAGTCATTGGC
TGCTATAGAGGCTTCTAGCTAAGGGAGTCCAATGTAAACAATTC
10 TAGAAGATAAGCATGTAGAGGTTAGCAGGGAGTTTGTCAAGGAC
GAGAGTTCGAGTCTCTCCACCTCCACCA SEQ ID NO: 161

Chlamydia pneumoniae (CWL029) tmRNA

GGGGGUGUAUAGGUUUCGACUUGAAAAUGAAGUGUUAUUGC
15 AUGCGGAGGGCGUUGGCUGGCCUCCUAAAAAGCCAACAAAACA
AUAUUAUGCCGAACCUAAGGCUGAAUGCGAAAUUAUUAAGCUUG
UUUGACUCAGUAGAGGAAAGACUAGCUGCUUAAUUAAGCAAAA
GUUGUUAGCUAGAUAAUCUCUAGGUAACCCGGUAUCUGCGAG
CUCCACCAGAGGCUUGCAAAAUACCGUCAUUUAUCUGGUUGGA
20 ACUUACUUUCUCUAAUUCUCAAGGAAGUUCGUUCGAGAUUUU
UGAGAGUCAUUGGCUGCUAUAGAGGCUUCUAGCUAAGGGAGU
CCAAUGUAAACAAUUCUAGAAGAUAAAGCAUGUAGAGGUUAGC
AGGGAGUUUGUCAAGGACGAGAGUUCGAGUCUCUCCACCUCCA
CCA SEQ ID NO: 162

Francisella tularensis *ssrA*

GGGGGCGAATATGGTTTCGACATGAATGTCAAAATCTAAGGTGC
ATGCCGAGGAAGTACCGTAACCTCGTTAATAACAGTACAAATGC
CAATAATAACTGGCAACAAAAAAGCAAACCGCGTAGCGGGCTAA
5 CGACAGCAACTTTGCTGCTGTTGCTAAAGCTGCCTAGTCTAGCTT
AATAATCTAGATGCGCACGGATATGATAGTCTTTCTTATGACACT
ATCTATACATCCGTTTCATATTCCGCATAAGACGGTCTTTGCTTTTT
GTCTGGGAGTTAAGGCTGTATTTAACAGACTCGCTAACTATTACC
CTGGCTAATTGGGGAATAGTCAAGCTAAACTCAAATAGATTAGC
10 CTAAGCATGTAGATCCAAAGATCTAGAGTTTGTGGACGCGGGGTT
CAAATCCCGCCGCCTCCACCA SEQ ID NO: 163

Francisella tularensis tmRNA

GGGGGCGAAUAUGGUUUCGACAUGAAUGUCAAAAUCUAAGGU
15 GCAUGCCGAGGAAGUACCGUAACCUCGUUAAUAACAGUACAAA
UGCCAAUAAUAACUGGCAACAAAAAAGCAAACCGCGUAGCGGC
UAACGACAGCAACUUUGCUGCUGUUGCUAAAGCUGCCUAGUCU
AGCUUAAUAAUCUAGAUGCGCACGGAUAUGAUAGUCUUUCUU
AUGACACUAUCUAUACAUCCGUUCAUAUUCCGCAUAAGACGGU
20 CUUUGCUIUUUUGUCUGGGAGUUAAGGCUGUAUUUAACAGACU
CGCUAACUAUUACCCUGGCUAAUUGGGGAAUAGUCAAGCUAA
ACUCAAAUAGAUUAGCCUAAGCAUGUAGAUCCAAAGAUCUAG
AGUUUGUGGACGCGGGGUUCAAUCCCGCCGCCUCCACCA
SEQ ID NO: 164

Guillardia theta (plastid) *ssrA*

GGGGCTGATTTGGATTCGACATATAAATTTGCGTGTTTCATTATG
AAGCAAGTCAAGTTTAATGATCTTGTAACAAACATTAAAGTACA
AATAAATGCAAGCAATATAGTTTCATTTAGTTCAAAACGTTTAGT
5 CTCTTTTGCATAAGCAAAATGTGTTAATAACTTTCTTAGTAGAAA
TTGGAGAAGTTTACTAAGATTTATATTTACTCCATAATTATTTTA
AAGATGGTAAAAAGGTGATTCATCATTGTATGTTTCTAAACTTT
GTGAAAGAATAGTGGGCTCCATTTATAATGAACGTGGGGTTCAAA
TCCCACCAGCTCCACCA SEQ ID NO: 165

10

Guillardia theta (plastid) tmRNA

GGGGCUGAUUUGGAUUCGACAUAAUAAAUUUGCGUGUUUCAUU
AUGAAGCAAGUCAAGUUUAAUGAUCUUGUAAAAACAUAUAAA
GUACAAAUAAAUGCAAGCAAUAUAGUUUCAUUUAGUUCAAAA
15 CGUUUAGUCUCUUUUGCAUAAGCAAAAUGUGUUAAUAACUUU
CUUAGUAGAAAUUGGAGAAGUUUACUAAGAUUUUAUAUUUACU
CCAUAUUUAUUUAAAGAUGGUAAAAAGGUGAUUCAUUAUU
GUAUGUUUCUAAACUUUGUGAAAGAAUAGUGGGGCUCCAUUUA
UAAUGAACGUGGGGUCAAAUCCCACCAGCUCCACCA
20 SEQ ID NO: 166

Thalassiosira Weissflogii (plastid) *ssrA*

GGGGCTGATTTGGTTTCGACATTTAAACTTCTTTCTATGTGTCA
GGTCAAAGTTTGTATTCTTTGTAAAAAAATACTAAAATACTAATA
25 AATGCTAATAATATAATACCGTTTATTTTTTAAAGCAGTAAAAAC

AAAAAAAGAAGCAATGGCTTTAAATTTTGCTGTATAGTTCATTA
ACTTAGGTTATTAAATATTTTTTCATTATAACTGGACTTTTCTCTA
GTTTATAGTTT TAGAATAAATTTAAATTTTGCAAAACTCGTTTCGAA
AATTTTCGGGCTAAACCTGTAAACGCAAATACTAAGAAATTTTA
5 GATGGACATGGGTTCAATTCCCATCAGTTCCACCA
SEQ ID NO: 167

Thalassiosira Weissflogii (plastid) tmRNA

GGGGCUGAUUUGGUUUCGACAUUUUAAAACUUCUUCUAUGUG
10 UCAGGUCAAAGUUUGUAUUCUUGUAAAAAAAAAUACUAAAAUA
CUAAUAAAUGCUAAUAUAUAUAUACCGUUUAUUUUUAAAGCA
GUAAAAACAAAAAAAGAAGCAAUGGCUUUUAAAUUUUGCUGUA
UAGUUCAUUAACUAGGUUAUUAUUUUUUUCAUUAUAAC
UGGACUUUUCUCUAGUUUAUAGUUUAGAAUAAAUUUUAAAUUU
15 UGCAAACUCGUUCGAAAAUUUUCGGGCUAAACCUGUAAACGC
AAAUACUAAGAAAUUUUAGAUGGACAUGGGGUCAAUUCCCAU
CAGUCCACCA SEQ ID NO: 168

20 *Helicobacter pylori* *ssrA*, (clinical isolate 1), internal partial

TGGGGATGTTACGGTTTCGACAGGGGTAGTTCGAGCTTAGGTGG
CGAGTCGAGGGGATCGGCCTCGTTAAAACGTCAAAGCCTATAAC
TGGCAAACAACAAAACAACCTTCGCTTTAGCAGCTTAATAAGCTC
TTAGCGGTTCCCTCCCTCCATCGCCCATGTGGTAGGGTAAGGGACT
25 CAAATTAAGTGGGCTACGCTGGATTCCACCGTCTGAGGATGAAA
GAAGAGAACAACCAGACTAGCTACCCGGACGCCCGTCGATAGG

CAGATGGAGTAGCGAATCGCGAATATATCGACTACACTCGTAGA
AGCTTAAGTGCCGATATTCTTGGACGTGGGTTCGACTCCC
SEQ ID NO: 176

5 *Helicobacter pylori* tmRNA, (clinical isolate 1), internal partial

UGGGGAUGUUACGGUUUCGACAGGGGUAGUUCGAGCUUAGGU
GGCGAGUCGAGGGGAUCGGCCUCGUUAAAACGUCAAAGCCUAU
AACUGGCAAACAACAAAACAACUUCGCUUUAGCAGCUUAAUAA
GCUCUUAGCGGUUCCUCCCUCCAUCGCCCAUGUGGUAGGGUAA
10 GGGACUCAAUUAAGUGGGCUACGCUGGAUUCCACCGUCUGAG
GAUGAAAGAAGAGAACAACCAGACUAGCUACCCGGACGCCCGU
CGAUAGGCAGAUUGGAGUAGCGAAUCGCGAAUAUAUCGACUAC
ACUCGUAGAAGCUUAAGUGCCGAUAUUCUUGGACGUGGGUUC
GACUCCC SEQ ID NO: 177

15

Helicobacter pylori ssrA, (clinical isolate 2), internal partial

TGGGGACGTTACGGTTTCGACAGGGATAGTTCGAGCTTAGGTTG
CGAGTCGAGGGGATCGGCCTCGTTAAACGTCAAAGCCTATAAT
20 TGGCAAACAAAACAATCTTTCTTTAGCTGCTTAATTGCACTAAAG
GTTCCCTCCCTCCATCGTCCATGTGGTAGGGTAAGGGACTCAAAC
AAGTGGACTACGCCGGAGTTCGCCGTCTGAGGACAAAGGAAGA
GAACAACCAGACTAGCAACTTGGAAGCCTGTCGATAGGCCGAAG
AGTTCGCGAAATGCTAATATATCGACTACACTCGTAGAAGCTTA
25 AGTGCCGATATTTTTGGACGTGGGTTCGATTCCCT SEQ ID NO:
178

Helicobacter pylori tmRNA, (clinical isolate 2), internal partial

UGGGGACGUUACGGUUUCGACAGGGAUAGUUCGAGCUUAGGU
UGCGAGUCGAGGGGAUCGGCCUCGUUAAAACGUCAAAGCCUAU
5 AAUUGGCAAACAAAACAAUCUUUCUUUAGCUGCUUAAUUGCA
CUAAAGGUUCCUCCCUCCAUCGUCCAUGUGGUAGGGGUAAGGGA
CUCAAACUAAGUGGACUACGCCGGAGUUCGCCGUCUGAGGACA
AAGGAAGAGAAACAACCAGACUAGCAACUUGGAAGCCUGUCGA
UAGGCCGAAGAGUUCGCGAAAUGC UAAUAUAUCGACUACACUC
10 GUAGAAGCUUAAGUGCCGAUAUUUUUGGACGUGGGUUCGAUU
CCCU SEQ ID NO: 179

Listeria seeligeri (NCTC 11856) *ssrA*, internal partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGGATCGTCC
15 TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA
AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
CCGTGCATCGCCCATGTGCTACGGAAAGGGTCTCACTTTAAGTG
GGCTACACTAAATAATCTCCGTCTGGGGGTTAGTTAGAAGAGCTT
AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA
20 TGCGAAATACTAATAACGGTGACTACGCTCGTAGATATTTAAGTG
CCCATATTTCTGG SEQ ID NO: 180

Listeria seeligeri (NCTC 11856) tmRNA, internal partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGGAUCGU
25 CCUCGUUAUCAACGUCAAAGCCAAUAUAACUGGCAAAGAAAA

ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG
AUCCUCCGUGCAUCGCCCAUGUGCUACGGAAAGGGUCUCACUU
UAAGUGGGGCUACACUAAAUAUCUCCGUCUGGGGGUUAGUUAG
AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG
5 CUGAUGUUUAUGCGAAAUACUAAUACGGUGACUACGCUCGUA
GAUAUUUAAGUGCCCAUAUUUCUGG SEQ ID NO: 181

Listeria ivanovii (NCTC 11846) *ssrA*, internal partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGGATCGTCC
10 TCGTTATTAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA
AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTTTAAGTGG
GCTACACTAAATAATCTCCGTCTGGGGTTAGTTAGAAGAGCTTA
ATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTAT
15 GCGAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTGC
CGATATTTCTGG SEQ ID NO: 182

Listeria ivanovii (NCTC 11846) tmRNA, internal partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGGAUCGU
20 CCUCGUUAUUAACGUCAAAGCCAUAUAUAAACUGGCAAAGAAA
AACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCU
GAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACU
UUAAGUGGGGCUACACUAAAUAUCUCCGUCUGGGGGUUAGUUA
GAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGG

GCUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUCGCUCGUA
GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 183

Mycobacterium africanum (clinical isolate) ssrA, internal partial

5 ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTCACA
TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC
AGACCGGGAACGCCCTCGGCCCGGACCCTGGCATCAGCTAGAGG
GATCCACCGATGAGTCCGGTCGCGGGACTCCTCGGGACAACCAC
10 AGCGACTGGGATCGTCATCTCGGCTAGTTCGCGTGACCGGGAGA
TCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAG
GGAATGCCGTA SEQ ID NO: 184

Mycobacterium africanum (clinical isolate) tmRNA, internal partial

15 ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCGACCAAUAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC
UGUCAGACCGGGAACGCCCU CGGCCCGGACCCUGGCAUCAGCU
AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUCGGGAC
20 AACCACAGCGACUGGGAUCGUCAUCUCGGCUAGUUCGCGUGAC
CGGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG
CCUUGAGGGAAUGCCGUA SEQ ID NO: 185

Mycobacterium gordonae(clinical isolate) *ssrA*, internal partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCAACCATATAAGCGCCGATTCACA
TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC
5 GGACCGGGAACGCCCTCGCCCCGGACCCCGGCATCAGCTAGAGG
GATCAACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCAAC
AGCGACTGGGATCGTCATCCTGGCTAGTCCGTGTGACCAGGAGA
TCCGAGCAGAGACATAGCGGACTGCGCACGGAGAAGCCTTGAG
GGAATGCCGTA SEQ ID NO: 186

10

Mycobacterium gordonae(clinical isolate) tmRNA, internal partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAUAUAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC
15 UGUCGGACCGGGAACGCCUCGCCCCGGACCCCGGCAUCAGCU
AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGACUCAUCGGGAC
ACCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUCCGUGUGAC
CAGGAGAUCCGAGCAGAGACAUAGCGGACUGCGCACGGAGAAG
CCUUGAGGGGAAUGCCGUA SEQ ID NO: 187

20

Mycobacterium kansasii (clinical isolate) *ssrA*, internal partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCAACCAAATAAGCGCCGATTCACA
TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC
25 AGACCGGGACCGCCCTCGACCCGGACTCTGGCATCAGCTAGAGG

GATCAACCGATGAGTTCGGTCGCGGGACTCGTCGGGACACCAAC
AGCGACTGGGATCGTCATCCTGGCTAGTTCGCGTGACCAGGAGA
TCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAG
GGAATGCCGTA SEQ ID NO: 188

5

Mycobacterium kansasii (clinical isolate) tmRNA, internal partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAAAUAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC
10 UGUCAGACCGGGACCGCCCUCGACCCGGACUCUGGCAUCAGCU
AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGACUCGUCGGGAC
ACCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUUCGCGUGAC
CAGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG
CCUUGAGGGGAAUGCCGUA SEQ ID NO: 189

15

Mycobacterium chelonae ssrA, internal partial

ACAGCGAGTCTCGACTTAAGGGAAGCGTGCCGGTGCAGGCAAG
AGACCACCGTAAGCGTCATTGCAACCAATTAAGCGCCGATTCTC
ATCAGCGCGACTACGCACTCGCTGCCTAAGCGACTGCGTGTCTG
20 TCAGACCGGGAGCGCCCTCAGCCCGGACCCTGGCATCAGCTAGA
GGGACAAACTACGGGTTCGGTCGCGGGACCCGTAGGGACATCAA
ACAGCGACTGGGATCGTCATCTCGGCTTGTTTCGCGGGACCGAGA
GATCCAAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTA
ATGAACGGCCGTTG SEQ ID NO: 190

25

Mycobacterium chelonae tmRNA, internal partial

ACAGCGAGUCUCGACUUAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCAUUGCAACCAAUUAAGCGCCGAUUCU
CAUCAGCGCGACUACGCACUCGCUGCCUAAGCGACUGCGUGUC
5 UGUCAGACCGGGAGCGCCCUCAGCCCGGACCCUGGCAUCAGCU
AGAGGGACAAACUACGGGUUCGGUCGCGGGACCCGUAGGGACA
UCAAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUCGCGGGAC
CGAGAGAUCCAAGUAGAGGCAUAGCGAACUGCGCACGGAGAA
GCCUUA AUGAACGGCCGUUG SEQ ID NO: 191

10

Mycobacterium szulgai (ATCC 35799) *ssrA*, internal partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGAGAACAC
TCAGCGCGACTTCGCTCTCGCTGCCTAAGCGACAGCAAGTCCGT
15 CAGACCGGGAAAGCCCTCGACCCGGACCCTGGCGTCATCTAGAG
GGATCCACCGGTGAGTTCGGTCGCGGGACTCATCGGGACACCAA
CAGCGACTGGGATCGTCATCCTGGCTAGTTCGCGTGACCAGGAG
ATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTTGA
GGGAATGCCGTAG SEQ ID NO: 192

20

Mycobacterium szulgai (ATCC 35799) tmRNA, internal partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAGAAC
ACUCAGCGCGACUUCGCUCUCGCUGCCUAAGCGACAGCAAGUC
25 CGUCAGACCGGGAAAGCCCUCGACCCGGACCCUGGCGUCAUCU

AGAGGGAUCCACCGGUGAGUUCGGUCGCGGGACUCAUCGGGAC
ACCAACAGCGACUGGGGAUCGUCAUCCUGGGCUAGUUCGCGUGAC
CAGGAGA UCCGAGUAGAGACA UAGCGAACUGCGCACGGAGAA
GCCUUGAGGGGAAUGCCGUAG SEQ ID NO: 193

5

Mycobacterium malmoeense (clinical isolate) ssrA, internal partial

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ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCAACCATATAAGCGCCGTTTCAAC
ACAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCGT
CAGACCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTGGAG
GGATCCACCGGTGAGTCCGGTCGCGGGACTCATCGGGACATACA
CAGCGACTGGGATCGTCATCCTGGCTGGTTCGCGTGACCGGGAG
ATCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGA
GGGAATGCCGTAG SEQ ID NO: 194

15

Mycobacterium malmoeense (clinical isolate) tmRNA, internal partial

20

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAUAUAAGCGCCGUUUCA
ACACAGCGCGACUACGCUCUCGCUGCCUAAGCGACAGCUAGUC
CGUCAGACCGGGAACGCCCU CGACCCGGAGCCUGGCGUCAGCU
GGAGGGAUCCACCGGUGAGUCCGGUCGCGGGACUCAUCGGGAC
AUACACAGCGACUGGGGAUCGUCAUCCUGGCUGGUUCGCGUGAC
CGGGAGA UCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG
CCUUGAGGGGAAUGCCGUAG SEQ ID NO: 195

25

Mycobacterium flavescens *ssrA*, internal partial

ACTTCGAGCGTCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAG
AGACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGATTCCA
ATCAGCGCGACTACGCACTCGCTGCCTAAGCGACTGCGTGTCTG
5 TCAGCCCGGGAGAGCCCTCGACCCGGTGTCTGGCATCAGCTAGA
GGGATAAACCGGTGGGTCCGGTCGCGGGACTCATCGGGACATCA
AACAGCGACTGGGATCGTCATCCTGACTTGTTGCGCGTGATCAGG
AGATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTT
GAGGGAACGCCGTAG SEQ ID NO: 196

10

Mycobacterium flavescens *tmRNA*, internal partial

ACUUCGAGCGUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAUUCC
AAUCAGCGCGACUACGCACUCGCGUGCCUAAGCGACUGCGUGUC
15 UGUCAGCCCGGGAGAGCCCUCGACCCGGUGUCUGGCAUCAGCU
AGAGGGAUAAACCGGUGGGUCCGGUCGCGGGACUCAUCGGGAC
AUCAAACAGCGACUGGGAUCGUCAUCCUGACUUGUUCGCGUGA
UCAGGAGAUCCGAGUAGAGACAUAGCGAACUGCGCACGGAGA
AGCCUUGAGGGAACGCCGUAG SEQ ID NO: 197

20

Mycobacterium marinum *ssrA*, internal partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGATGCAACTAGATAAGCGCCGATTCACA
25 TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC
GGACCGGGGAACGCCCTCGCCCCGGACCCCGGCATCAGCTAGAGG

GATCAACCGATGAGTTCGGTCGCGGGGCTCATCGGGACATCAAC
AGCGACTGGGATCGTCATCCTGGCTAGTTCGCGTGACCAGGAGA
TCCGAGCAGAGACCTAGCGGACTGCGCACGGAGAAGCCTTGAG
GGAATGCCGTAG SEQ ID NO: 198

5

Mycobacterium marinum tmRNA, internal partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGAUGCAACUAGAUAAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCGUGCCUAAGCGACGGCUAGUC
10 UGUCGGACCGGGAACGCCCUCGCCCCGGACCCCGGCAUCAGCU
AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGGCUCAUCGGGAC
AUCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUUCGCGUGAC
CAGGAGAUCCGAGCAGAGACCUAGCGGACUGCGCACGGAGAAG
CCUUGAGGGAAUGCCGUAG SEQ ID NO: 199

15

Mycobacterium microti (environmental isolate) ssrA, internal partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTCACA
TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC
20 AGACCGGGGAACGCCCTCGGCCCCGGACCCTGGCATCAGCTAGAGG
GATCCACCGATGAGTCCGGTCGCGGGACTCCTCGGGACAGCCAC
AGCGACTGGGATCGTCATCTCGGCTAGTTCGCGTGACCGGGAGA
TCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAG
GGAATGCCGTA SEQ ID NO: 200

25

Mycobacterium microti (environmental isolate) tmRNA, internal partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCGACCAAAUAAGCGCCGAUUCA
5 CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC
UGUCAGACCGGGAACGCCCUCGGCCCCGGACCCUGGCAUCAGCU
AGAGGGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUCGGGAC
AGCCACAGCGACUGGGGAUCGUCAUCUCGGCUAGUUCGCGUGAC
CGGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG
10 CCUUGAGGGGAAUGCCGUA SEQ ID NO: 201

Mycobacterium smegmatis (ATCC 10143) ssrA, internal partial

ACTTCGAGCATCGAATCCAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGATTCCAA
15 TCAGCGCGACTACGCCCTCGCTGCCTAAGCGACGGCTGGTCTGT
CAGACCGGGAGTGCCCTCGGCCCCGGATCCTGGCATCAGCTAGAG
GGACCCACCCACGGGTTCGGTCGCGGGACCTGTGGGGACATCAA
ACAGCGACTGGGATCGTCATCTCGGCTTGTTTCGTGTGACCGGGA
GATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTCG
20 AGGACATGCCGTAG SEQ ID NO: 202

Mycobacterium smegmatis (ATCC 10143) ssrA, internal partial

ACUUCGAGCAUCGAAUCCAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAUUCC
25 AAUCAGCGCGACUACGCCCUCGCUGCCUAAGCGACGGCUGGUC
UGUCAGACCGGGAGUGCCCUCGGCCCCGGAUCCUGGCAUCAGCU

AGAGGGACCCACCCACGGGUUCGGUCGCGGGACCUGUGGGGAC
AUCAAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUCGUGUGA
CCGGGAGAUCCGAGUAGAGACAUAGCGAACUGCGCACGGAGAA
GCCUCGAGGACAUGCCGUAG SEQ ID NO: 203

5

Mycobacterium xenopi (clinical isolate) *ssrA*, internal partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCAACTAAATAAGCGCCGATTCACA
TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCGT
10 CAGGCCGGGAGTTCCCTCGACCCGGATCCTGGCGTCAGCTAGAG
GGATCCACCGATGGGTTCGGTCGCGGGACCCATCGGGACACCAC
ACAGCGACTGGGATCGCCGTCCCGGCTAGTTCGCGAGACCGGGA
GATCCGAGTAAGGGCAAAGCGAACTGCGCACGGAGAAGCCTTG
AGGGTATGCCGTA SEQ ID NO: 204

15

Mycobacterium xenopi (clinical isolate) tmRNA, internal partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACUAAAUAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACAGCUAGUC
20 CGUCAGGCCGGGAGUUCCCUCGACCCGGAUCCUGGCGUCAGCU
AGAGGGAUCCACCGAUGGGGUUCGGUCGCGGGACCCAUCGGGAC
ACCACACAGCGACUGGGAUCGCCGUCCCGGCUAGUUCGCGAGA
CCGGGAGAUCCGAGUAAGGGCAAAGCGAACUGCGCACGGAGAA
GCCUUGAGGGGUAUGCCGUA SEQ ID NO: 205

25

Mycobacterium intracellulare (NCTC 10425) *ssrA*, internal partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACC
GACCACCGTAAGCGTCGTTGCAAACAGATAAGCGCCGATTCACA
TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCGT
5 CAGACCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTAGAG
GGATCCACCGATGAGTCCGGTCGCGGGACTTATCGGGACACCAA
CAGCGACTGGGATCGTCATCTCGGCTTGTTTCGCGTGACCGGGAG
ATCCGAGTAGAGGCATAGCGAACTGCGCACGGAGAAGTCTTGAG
GGAATGCCGTAG SEQ ID NO: 206

10

Mycobacterium intracellulare (NCTC 10425) tmRNA, internal partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAC
CGACCACCGUAAGCGUCGUUGCAAACAGAUAAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACAGCUAGUC
15 CGUCAGACCGGGAACGCCCUAGACCCGGAGCCUGGCGUCAGCU
AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUUAUCGGGAC
ACCAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUCGCGUGAC
CGGGAGAUCCGAGUAGAGGCAUAGCGAACUGCGCACGGAGAA
GUCUUGAGGGAAUGCCGUAG SEQ ID NO: 207

20

Mycobacterium scrofulaceum (NCTC 10803) *ssrA*, internal partial

ACATCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAG
AGACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGATTCAC
25 ATCAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCG
TCAGACCGGGAAGGCCCTCGACCCGGAGCCTGGCGTCAGCTAGA

GGGATCAACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCA
ACAGCGACTGGGATCGTCATCCTGGCTAGTCCGCGTGACCAGGA
GATCCGAGCAGAGGCATAGCGGACTGCGCACGGAGAAGTCTTG
AGGGAATGCCGTTG SEQ ID NO: 208

5

Mycobacterium scrofulaceum (NCTC 10803) tmRNA, internal partial

ACAUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACAGCUAGUC
10 CGUCAGACCGGGAAAGCCCUCGACCCGGAGCCUGGCGUCAGCU
AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGACUCAUCGGGAC
ACCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUCCGCGUGAC
CAGGAGAUCCGAGCAGAGGCAUAGCGGACUGCGCACGGAGAAG
UCUUGAGGGAAUGCCGUUG SEQ ID NO: 209

15

Nocardia asteroides ssrA, internal partial

ACTGTGTGCGCCGAGGTAGGGGAAGCGTGTCTGGTGCAGGCTGGA
GACCACCGTTAAGCGTCGCGGCAACCAATTAAGCGCCGATTCCA
ATCAGCGCGACTACGCCCTCGCTGCCTGATCAGCGACGGCTAGC
20 TGTCGGCCCCGGGTTGTGTTCCCGAACCCGGATGCCGGCATCATCT
CAGGGAACTCACCGTGTTCTGCCGGTCGCGGACGGACACGGGACA
GCAAACAGCGACTGGGATCGTCATCTCGGCTTGTTCTGCGTGACC
GGGAGATCCAAGTAGAGACATAGCGGACTGCACACGGAGAAGC
CCTACTGACTCGACACAG SEQ ID NO: 210

25

Nocardia asteroides tmRNA, internal partial

ACUGUGUGCGCCGAGGUAGGGGAAGCGUGUCGGUGCAGGCUG
GAGACCACCGUUAAGCGUCGCGGCAACCAAUUAAGCGCCGAUU
5 CCAAUCAGCGCGACUACGCCCUCGCUGCCUGAUCAGCGACGGC
UAGCUGUCGGCCCCGGGUUGUGUUCCCCGAACCCGGAUGCCGGCA
UCAUCUCAGGGAACUCACCGUGUUCGCCGGUCGCGGACGGACA
CGGGACAGCAAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUC
GCGUGACCGGGAGAUCCAAGUAGAGACAUAAGCGGCUGCACACG
10 GAGAAGCCCUACUGACUCGACACAG SEQ ID NO: 211

Salmonella enteritidis *ssrA*, internal partial

ACGGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGGCGGTTGGC
CTCGTAAAAAGCCGCAAAAAAATAGTCGCAAACGACGAAACCT
15 ACGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCTAG
CCTCCGCTCTTAGGACGGGGATCAAGAGAGGTCAAACCCAAAAG
AGATCGCGTGGATGCCCTGCCTGGGGTTGAAGCGTTAAAACGAA
TCAGGCTAGTCTGGTAGTGGCGTGTCCGTCCGCAGGTGCCAGGC
GAATGTAAAGACTGACTAAGCATGTAGTACCGAGGATGTAGGAA
20 TTTCGG SEQ ID NO: 212

Salmonella enteritidis tmRNA, internal partial

ACGGGAUUUGCGAAACCCAAGGUGCAUGCCGAGGGGGCGGUUG
GCCUCGUAAAAAGCCGCAAAAAAAUAGUCGCAAACGACGAAAC
25 CUACGCUUUAGCAGCUUAAUAACCUGCUUAGAGCCCUCUCUCC
CUAGCCUCCGCUCUUAGGACGGGGGAUCAAGAGAGGUCAAACCC

AAAAGAGAUCGCGUGGAUGCCCUGCCUGGGGUUGAAGCGUUA
AAACGAAUCAGGCUAGUCUGGUAGUGGCGUGUCCGUCCGCAGG
UGCCAGGCGAAUGUAAAGACUGACUAAGCAUGUAGUACCGAG
GAUGUAGGAAUUUCGG SEQ ID No: 213

5

Staphylococcus epidermidis (NCTC 11047) *ssrA*, internal partial

ACAGGGGTCCCCCGAGCTTATTAAGCGTGTCGGAGGGTGGCTC
CGTCATCAACACATTTTCGGTTAAATATAACTGACAAATCAAACA
ATAATTTTCGCAGTAGCTGCGTAATAGCCACTGCATCGCCTAACA
GCATCTCCTACGTGCTGTTAACGCGATTCAACCCTAGTAGGATAT
GCTAAACACTGCCGCTTGAAGTCTGTTTAGATGAAATATAATCA
AGCTAGTATCATGTTGGTTGTTTATTGCTTAGCATGATGCGAAAA
TTATCAATAAACTACACACGTAGAAAGATTTGTATCAGGACCTC
TGG SEQ ID NO: 214

15

Staphylococcus epidermidis (NCTC 11047) tmRNA, internal partial

ACAGGGGUCCCCCGAGCUUAUUAAGCGUGUCGGAGGGUUGGCU
CCGUCAUCAAACACAUUUCGGUUAUUAUUAACUGACAAAUCAA
CAAUAAUUUCGCAGUAGCUGCGUAAUAGCCACUGCAUCGCCUA
ACAGCAUCUCCUACGUGCUGUUAACGCGAUUCAACCCUAGUAG
GAUAUGCUAAACACUGCCGCUUGAAGUCUGUUUAGAUGAAAU
AUAAUCAAGCUAGUAUCAUGUUGGUUGUUUAUUGCUUAGCAU
GAUGCGAAAAUUAUCAAUAAACUACACACGUAGAAAGAUUUG
UAUCAGGACCUCUGG SEQ ID NO: 215

25

Streptococcus agalactiae (NCTC 8181) *ssrA*, internal partial

ACAGGCATTATGAGGTATATTTTGCGACTCATCGGCAGATGTAA
AATGCCAGTTAAATATAACTGCAAAAAATACAAATTCTTACGCA
TTAGCTGCCTAAAAAACAGCCTGCGTGATCTTCACAAGATTGTTT
5 GCGTTTTGCTAGAAGGTCTTATTTATCAGCAAACACTACGTTTGGCT
ACTGTCTAGTTAGTTAAAAAGAGATTTATAGACTCGCTATGTGA
GGGCTTGAGTTATGTGTCATCACCTAGTTAAATCAATACATAACC
TATAGTTGTAGACAAATATATTAGCAGATGTTTGG SEQ ID NO:
216

10

Streptococcus agalactiae (NCTC 8181) tmRNA, internal partial

ACAGGCAUUAUGAGGUUAUAUUUUGCGACUCAUCGGCAGAUGU
AAAAUGCCAGUUAAAUUAUACUGCAAAAAAUACAAAUUCUUA
CGCAUUAGCUGCCUAAAAAACAGCCUGCGUGAUCUUCACAAGA
15 UUGUUUGCGUUUUGCUAGAAGGUCUUAUUUAUCAGCAAACUA
CGUUUGGCUACUGUCUAGUUAGUUAAAAAGAGAUUUUAUAGAC
UCGCUAUGUGAGGGGCUUGAGUUAUGUGUCAUCACCUAGUUAA
AUCAAUACAUAACCUAUAGUUGUAGACAAAUUAUUUAGCAGA
UGUUUGG SEQ ID NO: 217

20

Of the above sequences SEQ ID NOs 47 to 62, 65 to 68, 71 and 72,
98 and 99, 159 to 168 and 176-217 are novel sequences.

The above mentioned sequences can be used to form a database of *ssrA* gene sequences which can be used to identify a bacterial species, or for the generation of nucleic acid diagnostic assays.

5 Representative probes identified in accordance with the invention are as follows:

Salmonella:

1) Genius specific probe:

10 5'-CGAATCAGGCTAGTCTGGTAG-3' SEQ ID NO: 218

Mycobacteria:

2) Oligonucleotide probe for detection of tuberculosis complex

15

TB01 5'-ACTCCTCGGACA (A/G) CCACAGCGA-3' SEQ ID NO: 219

3) Oligonucleotide probes for detection of *M. avium* and *M. paratuberculosis* sequences

20

Probe 1: PAV1 – 5' – GTTGCAAATAGATAAGCGCC-3' SEQ ID NO: 220

Probe 2: PAV2 – 5' – TCCGTCAGCCCGGGAACGCC-3' SEQ ID NO:

25

221

Listeria:

4) Oligonucleotide probe used in the determination of tmRNA integrity after heat killing treatment of cells:

5

LVtm: 5' - TTTTGTTTTTCTTTGCCA - 3' SEQ ID NO: 222

Escherichia coli:

10 5) Oligonucleotide probe used in the determination of tmRNA integrity after heat killing treatment of cells:

Evtm: 5' - AGTTTTCGTCGTTTGCGA - 3' SEQ ID NO: 223

15 Further representative primers identified in accordance with the invention are as follows:

Mycobacteria:

20 1) Degenerative oligonucleotide primers for the amplification of all mycobacterial sequences

5' Primer

10SAAM3 - 5' - CAGGCAA (G/C) (A/T/C) GACCACCGTAA-3' SEQ ID

25 NO: 224

3' Primer

10SAAM4 - 5' GGATCTCC(C/T)G(A/G)TC(A/T)C(A/G)CG(A/G)AC
(A/T)A-3' SEQ ID NO: 225

5

2) Oligonucleotide primers for the amplification of *M. avium* and *M. paratuberculosis*

5' Primer: AP1for- 5'-TGCCGGTGCAGGCAACTG-3' SEQ ID NO: 226

10 3' Primer: AP2rev - 5' - CACGCGAACAAGCCAGGA-3' SEQ ID NO:
227

Brief Description of the Drawings

15 In the accompanying drawings:

Fig. 1 is a clustal alignment of *E. coli* and *V. cholerae* *ssrA* gene sequences;

20 Fig. 2 is a photograph of an agarose gel of total cellular RNA prepared from *E. coli* and *V. cholerae* cells;

Fig. 3 is a photograph of an autoradiogram of hybridisation of a *V. cholerae* oligonucleotide probe to tmRNA transcripts of *E. coli* and *V. cholerae*;
25

Fig. 4 is a photograph of an agarose gel of the amplified products of universal *ssrA* gene amplification primers from a panel of organisms;

Fig. 5 is a clustal alignment of the *ssrA* gene sequences from the
5 *Listeria* species;

Fig. 6 is a clustal alignment of the *L. monocytogenes* and *B. subtilis* *ssrA*/tmRNA gene sequences;

10 Fig. 7 is a photograph of an agarose gel of the amplified products of *Listeria* genus specific PCR amplification primers from a panel of organisms;

Fig. 8 is a photograph of an autoradiogram of hybridised *Listeria*
15 genus specific oligonucleotide probe to a panel of organisms as prepared in Example 4;

Fig. 9 is a photograph of an autoradiogram of hybridised *L. monocytogenes* species specific probe to a panel of organisms as prepared
20 in Example 7;

Fig. 10 is a computer scanned image of a nylon membrane strip used in the multiple colorimetric probe detection of *Listeria ssrA* gene sequences as described in Example 6.

Fig. 11 is a clustal alignment of *ssrA* gene sequences from *C. trachomatis* strains;

Fig. 12 is a clustal alignment of *ssrA* gene sequences from *H. pylori* strains;

Fig. 13 is a clustal alignment of *ssrA* gene sequences from *M. genitalium* strains;

Fig. 14 is a clustal alignment of *ssrA* gene sequences from *N. gonorrhoeae* strains;

Fig. 15 is a clustal alignment of *ssrA* gene sequences from *L. monocytogenes* strains;

Fig. 16 is a clustal alignment of *ssrA* gene sequences from *L. monocytogenes* strains and the *L. innocua* strain;

Fig. 17 is a photograph of an autoradiogram hybridised *Listeria* oligonucleotide probe (Evtm) to total RNA samples isolated after medium heat treatment of *E. coli* cells;

Fig. 18 is a photograph of an autoradiogram hybridised *Listeria* oligonucleotide probe (Evtm) to total RNA samples isolated after extreme heat treatment of *E. coli* cells;

Fig. 19 is a photograph of an autoradiogram hybridised Listeria oligonucleotide probe (Lvtm) to total RNA samples isolated after medium heat treatment of *L. monocytogenes* cells;

5 Fig. 20 is a photograph of an autoradiogram hybridised Listeria oligonucleotide probe (Lvtm) to total RNA samples isolated after extreme heat treatment of *L. monocytogenes* cells; and

10 Fig. 21 is a photograph of an agarose gel of RT-PCR generated tmRNA products at various time points post heat treatment.

The invention will be further illustrated by the following Examples.

Modes for carrying out the Invention

15

Example 1

Examination of the primary nucleotide sequences of available tmRNA sequences.

20

A comparative primary nucleotide sequence alignment of available tmRNA sequences using the Clustal W nucleic acid alignment programme demonstrated that tmRNA sequences from prokaryotes show a more significant degree of nucleotide sequence variability and non-homology
25 than other bacterial high copy number RNA, as demonstrated in Table 1.

Table 1

Percentage nucleotide sequence homology between RNA molecules from
different bacteria.

5

	<i>Escherichia coli</i> vs. <i>Vibrio cholerae</i>	<i>Bacillus subtilis</i> vs. <i>Mycobacterium tuberculosis</i>
rRNA % homology	88	66
tmRNA % homology	68	25

These regions of non-homology between tmRNA sequences from
different bacteria are located in the middle of the molecule, and the extent
of nucleotide sequence non-homology within the tmRNA molecule
10 indicated that genus as well as species specific probes could be generated to
distinguish between and/or detect bacteria.

Nucleotide sequence alignments had previously shown that the 5' and
3' flanking regions of the tmRNA molecules share a high degree of
15 homology both within species and within genus. This observation indicated
that universal oligonucleotide primers could be generated to amplify the
ssrA gene or its encoding tmRNA from a wide variety of bacteria.

We have now demonstrated that these regions of homology and non-
20 homology within the nucleotide sequence of tmRNA molecules from

different organisms can be used as the basis of identifying and detecting organisms at the molecular level.

Example 2

5

Development of a *V. cholerae* tmRNA specific probe.

A nucleotide sequence alignment of the *E. coli* (SEQ ID NO. 37) and *V. cholerae* (SEQ ID NO. 127) *ssrA* sequences as depicted in Fig. 1, shows that these two bacterial species are phylogenetically closely related. There are however, regions of non-homology between the sequences as evidenced by the absence of asterix marks. An oligonucleotide probe, complementary to the variable region of the *V. cholerae* *ssrA* nucleotide sequence underlined in Fig. 1, was synthesised.

15

The sequence of the *V. cholerae* tmRNA specific probe is

5'- AACGAATGGCTAACCTGAA-3' SEQ ID NO. 169

20

Total RNA was isolated from liquid cultures of *E. coli* and *V. cholerae* at the mid-exponential phase and the stationary phase of growth. Equivalent amounts of the isolated total RNA were electrophoresed on a denaturing formaldehyde agarose gel and blotted onto HYBOND-N nylon membrane as shown in Fig. 2 in which the Lanes 1-4 represent the following:

25

Lane 1: Total *E. coli* RNA mid-log phase
Lane 2: Total *V. cholerae* RNA mid-log phase
Lane 3: Total *E. coli* RNA stationary phase
Lane 4: Total *V. cholerae* RNA stationary phase

5

The resulting Northern blot was then hybridised with the *V. cholerae* tmRNA specific probe end-labelled with γP^{32} . The results of the hybridisation experiment shown in Fig. 3 demonstrate the specificity of the probe as only *V. cholerae* tmRNAs were detected. Moreover, a greater degree of hybridisation signal intensity was observed with the *V. cholerae* tmRNA isolated from cultures during the stationary phase of growth, indicating that a higher copy number of the tmRNA molecule is present in *V. cholerae* cells during this phase.

10

Example 3

Generation of universal ssrA/tmRNA oligonucleotide amplification primers for the characterisation of unknown ssrA gene and tmRNA sequences.

15

Clustal W alignment of all available ssrA gene and tmRNA sequences indicated that degenerate oligonucleotide primers could be designed to amplify ssrA gene and tmRNA nucleotide sequences for a wide variety of organisms.

20

The sequences of the synthesised degenerate oligonucleotides are as follows:

(a) tmU5': 5' *in vitro* PCR amplification primer
5'- GGG(A/C)(C/T)TACGG(A/T)TTCGAC- 3'
SEQ ID NO: 170

(b) tmU3': 3' *in vitro* PCR amplification primer
5'- GGGA(A/G)TCGAACC(A/G)(C/G)GTCC- 3'
SEQ ID NO: 171

Degenerate base positions are in parentheses.

The products of PCR reactions were electrophoresed on an agarose gel and a 350 base pair (approx.) PCR product was amplified in all cases, as shown in Fig. 4, demonstrating the “universality” of the degenerate tmRNA primers.

In Fig. 4 the lanes represent the following:

	Lane A:	Molecular weight marker V
	Lane 1:	<i>Escherichia coli</i>
5	Lane 2:	<i>Salmonella poona</i>
	Lane 3:	<i>Klebsiella aerogenes</i>
	Lane 4:	<i>Proteus mirabilis</i>
	Lane 5:	<i>Proteus rettgeri</i>
	Lane 6:	<i>Aeromonas hydrophilia</i>
10	Lane 7:	<i>Staphylococcus aureus</i>
	Lane 8:	<i>Enterococcus faecalis</i>
	Lane 9:	<i>Lactobacillus lactis</i>
	Lane 10:	<i>Bacillus subtilus</i>
	Lane 11:	<i>Listeria monocytogenes</i>
15	Lane 12:	<i>Listeria innocua</i>
	Lane 13:	<i>Listeria murrayi</i>
	Lane 14:	<i>Listeria welshimeri</i>
	Lane 15:	<i>Listeria grayi</i>
	Lane 16:	<i>Mycobacterium bovis</i>
20	Lane B:	Molecular weight marker V

The universal primers amplified the *ssrA* gene from both Gram positive and Gram negative bacteria, as shown in Table 2.

Table 2Bacterial species tested with universal amplification primers.

		PCR Product
Gram negative bacteria	<i>Escherichia coli</i>	+
	<i>Salmonella poona</i>	+
	<i>Klebsiella aerogenes</i>	+
	<i>Proteus mirabilis</i>	+
	<i>Proteus rettgeri</i>	+
	<i>Aeromonas hydrophilia</i>	+
Gram positive bacteria	<i>Staphylococcus aureus</i>	+
	<i>Enterococcus faecalis</i>	+
	<i>Lactobacillus lactis</i>	+
	<i>Bacillus subtilus</i>	+
	<i>Listeria monocytogenes</i>	+
	<i>Listeria innocua</i>	+
	<i>Listeria murrayi</i>	+
	<i>Listeria welshimeri</i>	+
	<i>Listeria grayi</i>	+
	<i>Mycobacterium bovis</i>	+

Example 4Isolation and characterisation of previously unknown bacterial ssrA/tmRNA
nucleotide sequences.

5

The PCR products amplified from genomic DNA from the *Listeria* species of bacteria and that from the *M. bovis* bacterium, from Example 2, were subcloned into a T-tailed plasmid vector for the purposes of DNA sequencing. Three recombinant clones were selected for each species and
10 sequenced by the di-deoxy sequencing method. The sequence of both DNA strands for each subclone was determined.

The nucleotide sequence determined for the *M. bovis* ssrA gene shared 100% homology with the *Mycobacterium tuberculosis* ssrA gene
15 sequence.

A clustal W alignment of the novel ssrA gene sequences obtained for the *Listeria* species (SEQ ID NOS 51, 53, 55, 59 and 61) is shown in Fig. 5. This analysis indicated that genus-specific probes and oligonucleotide
20 amplification primers can be generated for *Listeria* bacteria. Furthermore, the alignment also indicated that a species specific oligonucleotide probe can be generated which will distinguish *L. monocytogenes* from the other *Listeria* species.

In Fig. 5 the proposed genus specific oligonucleotide primers, Ltm 1 and Ltm 2, are boxed, as is the genus specific *Listeria* oligonucleotide probe, LGtm. The proposed *L. monocytogenes* species specific oligonucleotide probe sequence, LStm, is underlined and italicised.

5

To further illustrate that the *ssrA* gene/tmRNA nucleic acid target is a suitable target for bacterial diagnostics, a comparative alignment of the *L. monocytogenes* *ssrA* gene nucleotide sequence (SEQ ID NO. 55) with the available *B. subtilis* *ssrA* gene nucleotide sequence (SEQ ID NO. 11) (a phylogenetically closely related bacteria to *Listeria*) was carried out as shown in Fig. 6. Analysis of the sequence alignment showed a percentage nucleotide sequence homology of 41%, whereas the corresponding 16S rRNA alignment exhibits a nucleotide sequence percentage homology of 87%, (data not shown).

10
15

Example 5

Generation and application of *ssrA* gene/tmRNA genus-specific amplification primers, genus-specific and species-specific probes for the
Listeria bacterial species.

20

Using the *Listeria* genus *ssrA* gene/tmRNA nucleotide sequence alignment of Example 4, regions of the *ssrA* gene/tmRNA nucleotide sequence were analysed to determine their suitability for the generation of genus-specific amplification primers, and genus-specific and species-

25

specific oligonucleotide probes. In this analysis , regions which demonstrated the greatest sequence differences to *B. subtilis*, were selected in the design of these amplification primers and probes.

5 The sequences of the synthesised oligonucleotides are as follows:

(a) Ltm1: 5' Listeria genus specific amplification primer
 5' -AAAGCCAATAATACTGG- 3'
 SEQ ID NO: 172

10

(b) Ltm2: 3' Listeria genus specific amplification primer
 5' -CCAGAAATATCGGCACTT- 3'
 SEQ ID NO: 173

15

(c) LGtm: Listeria genus specific hybridisation probe
 5' -GTGAGACCCTTACCGTAG- 3'
 SEQ ID NO: 174

20

(d) LStm: *L. monocytogenes* species specific hybridisation
 probe
 5' -TCTATTTAACCCCAGACG- 3'
 SEQ ID NO: 175

25 The genus specific amplification primers Ltm1 and Ltm2 were used
 in a series of PCR reactions with total genomic DNA from twenty different

strains as the template in each case. Only *ssrA* gene sequences from the *Listeria* species were amplified (260 base pair product) with these primers (Fig. 7 and Table 3) demonstrating that the *ssrA* gene/tmRNA is a suitable target for specific *in vitro* amplification of a bacterial genus. No
5 amplification products were observed for any other bacterial species tested, although PCR products were obtained from the DNA from these bacterial species using the universal primers (tmU5' and tmU3') described in Example 2.

10 In Fig. 7 the lanes represent the following:

- Lane A: Molecular weight marker V
- Lane 1: *E. coli*
- Lane 2: *S. poona*
- 15 Lane 3: *K. aerogenes*
- Lane 4: *P. mirabilis*
- Lane 5: *P. rettgeri*
- Lane 6: *A. hydrophilia*
- Lane 7: *S. aureus*
- 20 Lane 8: *E. faecalis*
- Lane 9: *L. lactis*
- Lane 10: *B. subtilis*
- Lane 11: *L. monocytogenes* strain 1
- Lane 12: *L. monocytogenes* strain 2
- 25 Lane 13: *L. monocytogenes* strain 3

- Lane 14: *L. monocytogenes* strain 4
- Lane 15: *L. monocytogenes* clinical isolate
- Lane 16: *L. innocua*
- Lane 17: *L. murrayi*
- 5 Lane 18: *L. welshimeri*
- Lane 19: *L. grayi*
- Lane 20: *M. bovis*
- Lane B: Molecular weight marker V

Table 3Bacterial species tested with Listeria specific amplification primers.

		PCR Product
Gram negative bacteria	<i>Escherichia coli</i>	-
	<i>Salmonella poona</i>	-
	<i>Klebsiella aerogenes</i>	-
	<i>Proteus mirabilis</i>	-
	<i>Proteus rettgeri</i>	-
	<i>Aeromonas hydrophilia</i>	-
Gram positive bacteria	<i>Staphylococcus aureus</i>	-
	<i>Enterococcus faecalis</i>	-
	<i>Lactobacillus lactis</i>	-
	<i>Bacillus subtilis</i>	-
	<i>Listeria monocytogenes</i> strain 1	+
	<i>Listeria monocytogenes</i> strain 2	+
	<i>Listeria monocytogenes</i> strain 3	+
	<i>Listeria monocytogenes</i> strain 4	+
	<i>Listeria monocytogenes</i> clinical isolate	+
	<i>Listeria innocua</i>	+
	<i>Listeria murrayi</i>	+
	<i>Listeria welshimeri</i>	+
	<i>Listeria grayi</i>	+
	<i>Mycobacterium bovis</i>	-

The *Listeria* genus specific oligonucleotide probe, LGtm, was hybridised to the Southern blot depicted in Fig. 4. Positive hybridisation signals were observed only with *Listeria* species as shown in Fig. 8 and Table 4, demonstrating the utility of the tmRNA sequence as a target in
5 detecting a specific genus.

In Fig. 8 the lanes represent the following:

- | | | |
|----|----------|-------------------------------|
| 10 | Lane A: | Molecular weight marker V |
| | Lane 1: | <i>Escherichia coli</i> |
| | Lane 2: | <i>Salmonella poona</i> |
| | Lane 3: | <i>Klebsiella aerogenes</i> |
| | Lane 4: | <i>Proteus mirabilis</i> |
| 15 | Lane 5: | <i>Proteus rettgeri</i> |
| | Lane 6: | <i>Aeromonas hydrophilia</i> |
| | Lane 7: | <i>Staphylococcus aureus</i> |
| | Lane 8: | <i>Enterococcus faecalis</i> |
| | Lane 9: | <i>Lactobacillus lactis</i> |
| 20 | Lane 10: | <i>Bacillus subtilis</i> |
| | Lane 11: | <i>Listeria monocytogenes</i> |
| | Lane 12: | <i>Listeria innocua</i> |
| | Lane 13: | <i>Listeria murrayi</i> |
| | Lane 14: | <i>Listeria welshimeri</i> |
| 25 | Lane 15: | <i>Listeria grayi</i> |
| | Lane 16: | <i>Mycobacterium bovis</i> |

Lane B: Molecular weight marker V

The PCR products generated using the genus-specific amplification described in this Example, and shown in Fig. 7, were Southern blotted and hybridised to the *L. monocytogenes* species-specific oligonucleotide probe. A positive hybridisation signal was observed with three of the four typed strains and the clinical isolate of *L. monocytogenes* as shown in Fig. 9 and Table 4.

In Fig. 9 the lanes represent the following:

Lane A: Molecular weight marker V

Lane 1: *E. coli*

Lane 2: *S. poona*

Lane 3: *K. aerogenes*

Lane 4: *P. mirabilis*

Lane 5: *P. rettgeri*

Lane 6: *A. hydrophilia*

Lane 7: *S. aureus*

Lane 8: *E. faecalis*

Lane 9: *L. lactis*

Lane 10: *B. subtilis*

Lane 11: *L. monocytogenes* strain 1

Lane 12: *L. monocytogenes* strain 2

Lane 13: *L. monocytogenes* strain 3

- Lane 14: *L. monocytogenes* strain 4
- Lane 15: *L. monocytogenes* clinical isolate
- Lane 16: *L. innocua*
- Lane 17: *L. murrayi*
- 5 Lane 18: *L. welshimeri*
- Lane 19: *L. grayi*
- Lane 20: *M. bovis*
- Lane B: Molecular weight marker V

Table 4

Specificity of the Listeria genus-specific probe and the *L. monocytogenes* species-specific probe.

5

		LGtm Genus- specific probe	LStm Species- specific probe
Gram negative bacteria	<i>Escherichia coli</i>	-	-
	<i>Salmonella poona</i>	-	-
	<i>Klebsiella aerogenes</i>	-	-
	<i>Proteus mirabilis</i>	-	-
	<i>Proteus rettgeri</i>	-	-
	<i>Aeromonas hydrophilia</i>	-	-
Gram positive bacteria	<i>Staphylococcus aureus</i>	-	-
	<i>Enterococcus faecalis</i>	-	-
	<i>Lactobacillus lactis</i>	-	-
	<i>Bacillus subtilis</i>	-	-
	<i>Listeria monocytogenes</i> strain 1	+	+
	<i>Listeria monocytogenes</i> strain 2	+	+
	<i>Listeria monocytogenes</i> strain 3	+	+
	<i>Listeria monocytogenes</i> strain 4	+	-
	<i>Listeria monocytogenes</i> clinical isolate	+	+
	<i>Listeria innocua</i>	+	-
	<i>Listeria murrayi</i>	+	-
	<i>Listeria welshimeri</i>	+	-
	<i>Listeria grayi</i>	+	-
	<i>Mycobacterium bovis</i>	-	-

One of the typed *L. monocytogenes* strains, strain 4, failed to generate a positive signal with this probe. DNA sequencing of the PCR amplified *ssrA* gene from this strain demonstrated that it contained a probe target region identical to *L. innocua*. It should be noted however that the *ssrA* gene from this strain contains other regions where the sequence is identical to the previously characterised *L. monocytogenes* strain and that these sequences are different to the *L. innocua* sequence, as shown in Fig. 15. Therefore a species specific oligonucleotide directed to one of these variable regions can be synthesised which would recognise each strain type (isolate) within the species, for example *L. monocytogenes*.

Example 6

Multiple colorimetric probe detection of *Listeria ssrA* gene sequences.

15

LGTm (A), LStm (B) and a *Campylobacter upsaliensis* 16S - 23S rRNA spacer (C - 5' CATTAAGCTTTAGCAAGGAAGTG 3') SEQ ID NO: 228 oligonucleotide probe were irreversibly bound to nylon membrane strips and hybridised to with amplified *ssrA* PCR product, using the genus specific primers Ltm1 and Ltm2 (Ltm1 was labelled with biotin at the 5' end), from *L. monocytogenes* (1-6), *L. innocua* (7-10), *L. ivanovii* (11), *L. murrayi* (12), *L. seeligeri* (13), *L. welshmeri* (14) and *L. grayii* (15). The *ssrA* amplified PCR products, using tmU5' and tmU3' (tmU5' was labelled with biotin at the 5' end), were also hybridised to the nylon membrane strips from the Gram-positive bacteria, *B. subtilis*, *L. lactis*, *S. aureus*, *S.*

25

epidermis, *E. faecalis*, *C. perfringens* (16-21) and the Gram-negative bacteria *E. coli*, *S. enteritidis*, *P. Rettgeri*, *K. aerogenes* (22-25). As shown in Fig. 10 after hybridisation, development of the colorimetric assay to biotin revealed the following: Strips 1-6 demonstrates that the *ssrA* amplified PCR product originated from *L. monocytogenes* combined with the confirmation that the PCR product amplified is from the genus *Listeria* - A and B give colour detection; Strips 7 - 15 demonstrate that these PCR products originated from the genus *Listeria* - only A gives colour detection; and Strips 16 - 25 demonstrate that the PCR products are not from the genus *Listeria* - no colour detection. C is a negative oligonucleotide control probe and D is a positive control colorimetric detection assay for all samples.

Example 7

15

Use of *ssrA* / tmRNA sequences to distinguish between species of organisms.

Clustal W alignments as shown in Figs. 11 (SEQ ID NOS. 19 and 21), 12 (SEQ ID NOS. 41 and 43), 13 (SEQ ID NOS. 77 and 79), 14 (SEQ ID NOS. 83 and 85), 15 and 16 (SEQ ID NO. 53, 55 and 57), indicate that there are nucleotide differences within the *ssrA*/tmRNA sequences of different strains of the same bacteria. This suggests that the *ssrA*/tmRNA sequences could potentially be used to discriminate between individual

and/or groups of strains within a bacterial species. This may have useful applications in epidemiology and bacterial population analysis.

Example 8

5

tmRNA integrity analysis after medium and extreme heat treatment of bacterial cells.

E. coli and *L. monocytogenes* cultures were heat treated at 80°C , for 20
10 min. in the case of *E. coli* and 40 min. in the case of *L. monocytogenes* and
at 120°C for 15 min. (autoclaving) after overnight growth and tested for
viability at 0h, 1h, 2h, 6h, 12h, 24h and 48h after heat treatment. No
viability was observed at each time period tested. Total RNA was also
isolated at these time periods and electrophoresed on denaturing 1.2%
15 agarose gels and Northern blotted. Each blot was hybridised to, in the case
of *E. coli* (Figs. 17 and 18) with a radioactively labelled oligonucleotide
probe Evtm and in the case of *L. monocytogenes* (Figs. 19 and 20) with a
radiolabelled LVtm. No tmRNA transcript was detected with each sample
tested, demonstrating that tmRNA transcript is degraded after heat
20 treatment. The lanes represented with the notation +ve is a positive control
total RNA sample.

Example 9Use of the tmRNA transcript in distinguishing between viable and non-viable bacteria.

5

A 100 ml culture of *L. monocytogenes* was grown overnight in liquid culture. After growth, serial dilutions of the cells were carried out and viability was determined by spread plating on nutrient agar plates.

Simultaneously, total RNA was isolated from a 1 ml aliquot of these cells.

10 The remainder of the cells were heated at 65°C for 20 min. Cells were then removed for both viability analysis and total RNA isolation. Samples were taken for viability and RNA isolation at time periods of 0 h, 2 h, 6 h and 24 h after treatment.

15 Spread plating on nutrient agar plates indicated that heat treatment killed *L. monocytogenes* cells, with no viable colony forming units observed. Each RNA sample isolated was then treated with DNase to remove any contaminating DNA and total RNA samples (100 ng) were subjected to Reverse Transcriptase-PCR amplification using the *Listeria*
20 genus specific *ssrA*/tmRNA oligonucleotide primers Ltm1 and Ltm2. Negative control amplification reactions included primers, target, and Taq polymerase, but no Reverse Transcriptase. The results of the amplification reactions are shown in Fig. 12.

Amplified tmRNA RT-PCR products were only observed with the RNA sample which was not heat treated. All other samples gave no RT-PCR product indicating that the tmRNA molecules in these samples may have been degraded in the non-viable heat treated cells.

5

In Fig. 21 the lanes represent the following:

- | | | |
|----|----------|--|
| | Lane A: | Molecular weight marker V; |
| | Lane 1: | PCR amplification of RNA (no heat treatment of cells) |
| 10 | | - Reverse Transcriptase (RT), + Taq polymerase (TP); |
| | Lane 2: | RT-PCR of RNA (no heat treatment of cells), + RT, +TP; |
| | Lane 3: | PCR amplification of RNA (at 0 time after heat treatment), |
| | | -RT, +TP; |
| | Lane 4: | RT-PCR of RNA (at 0 time after heat treatment), +RT, +TP; |
| 15 | Lane 5: | PCR amplification of RNA (at 1 h time after heat treatment), |
| | | -RT, +TP; |
| | Lane 6: | RT-PCR of RNA (at 1 h time after heat treatment), |
| | | +RT, +TP; |
| | Lane 7: | PCR amplification of RNA (at 2 h time after heat treatment), |
| 20 | | -RT, +TP; |
| | Lane 8: | RT-PCR of RNA (at 2 h time after heat treatment), |
| | | +RT, +TP; |
| | Lane 9: | PCR amplification of RNA (at 6 h time after heat treatment), |
| | | -RT, +TP; |
| 25 | Lane 10: | RT-PCR of RNA (at 6 h time after heat treatment), |

+RT, +TP;

Lane 11: PCR amplification of RNA (at 24 h time after heat treatment),
-RT, +TP;

Lane 12: RT-PCR of RNA (at 24 h time after heat treatment),
+RT, +TP;

5

Lane B: Molecular weight marker V.

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __2__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __2__

NOTE: For additional volumes please contact the Canadian Patent Office.

Claims:

1. Use of the *ssrA* gene or a fragment thereof consisting of at least ten nucleotides as a target region in a nucleic acid probe assay for a prokaryotic
5 or eukaryotic organism.
2. Use according to Claim 1, wherein the fragment of the *ssrA* gene has a sequence corresponding to a region of high homology from the 5' end of the DNA molecule and is used as a universal target region.
10
3. Use according to Claim 1, wherein the fragment of the *ssrA* gene has a sequence corresponding to a region of high homology from the 3' end of the DNA molecule and is used as a universal target region.
- 15 4. Use according to Claim 1, wherein the fragment of the *ssrA* gene has a sequence corresponding to a region of low homology and is used as a target region in a nucleic acid probe assay to distinguish between species.
- 20 5. Use according to Claim 1, wherein the fragment of the *ssrA* gene has a sequence corresponding to a region of low homology and is used as a target region for the generation of a genus specific probe.
6. Use of tmRNA, an RNA transcript of the *ssrA* gene, or a fragment thereof consisting of at least ten nucleotides as a target region in a nucleic
25 acid probe assay for a prokaryotic or eukaryotic organism.

7. Use according to Claim 6, wherein the fragment of the tmRNA has a sequence corresponding to a region of high homology from the 5' end of the tmRNA molecule and is used as a universal target region.
- 5 8. Use according to Claim 6, wherein the fragment of the tmRNA has a sequence corresponding to a region of high homology from the 3' end of the tmRNA molecule and is used as a universal target region.
9. Use according to Claim 6, wherein the fragment of the tmRNA has a
10 sequence corresponding to a region of low homology and is used as a target region in a nucleic acid probe assay to distinguish between species.
10. Use according to Claim 6, wherein the fragment of the tmRNA has a
15 sequence corresponding to a region of low homology and is used as a target region for the generation of a genus specific probe.
11. Use according to any one of Claims 1 to 10, wherein said ssrA gene fragment or said tmRNA fragment is used as the basis of a primer to be used in an amplification procedure.
- 20 12. Use according to Claim 11, wherein the product of the amplification procedure is used as a target region in a nucleic acid probe assay.
13. Use according to any one of Claims 6 to 12, wherein a cDNA
25 transcript of the tmRNA molecule is used as a probe in a nucleic acid hybridisation assay.

14. Use according to any one of Claims 1 to 13, where the assay is carried out *in vitro*.

15. Use according to any one of Claims 1 to 13, where the assay is
5 carried out *in situ*.

16. Use according to any one of Claims 1 to 15, wherein the target region is used as the basis of an assay for distinguishing between living and dead prokaryotic or eukaryotic organisms.

10

17. Use according to any one of Claims 1 to 16, wherein the target region is used in a multiple probe format for broad scale detection and/or identification of prokaryotic or eukaryotic organisms.

15 18. Use according to Claim 17, wherein an *ssrA* gene probe or a *tmRNA* transcript probe is linked to a microarray gene chip system for the broad scale high throughput detection and identification of prokaryotic or eukaryotic organisms.

20 19. Use according to any one of Claims 1 to 18, wherein the target region is used as a probe in an assay to detect prokaryotic or eukaryotic organisms in a sample of matter.

20. Use according to any one of Claims 1 to 13, wherein a fragment of
25 the *ssrA* gene or the *tmRNA* transcript is used in an assay to obtain a DNA profile of a prokaryotic or eukaryotic organism and, thereby, distinguish between strains of the same species.

21. Use according to any one of Claims 1 to 13, wherein the *ssrA* gene, the tmRNA transcript or a DNA sequence complementary thereto, or a fragment thereof, is used to design an agent directed against infectious
5 prokaryotic or eukaryotic organisms for therapeutic purposes.
22. Use according to any one of Claims 1 to 15, wherein the target region is used to monitor the efficacy of drug therapies against infectious agents.
- 10 23. Use according to any one of Claims 1 to 15, wherein the target region is used to monitor the viability and level of health-promoting organisms in the gastrointestinal tract.
24. Use according to any one of Claims 1 to 15, wherein the assay is used
15 for the quantification of prokaryotic or eukaryotic organisms.
25. Use according to any one of Claims 1 to 5 and 11 to 15, wherein a database of *ssrA* gene sequences is used to identify a prokaryotic or eukaryotic organism.

E. c.	GGGGCTGATTCTGGATTTCGACGGGATTTCGGAAACCCAAAGGTGCATGCCG
V. c.	GGGGCTGATTTCAGGATTTCGACGGGAATTTTGCAGTCTGAGGTGCATGCCG

E. c.	AGGGCGGTTGGCCTCGTAAA - AAGCCGCAAAAAA - TAGTCGCAAAACGAC
V. c.	AGGTGCGGTAGGCCCTCGTTAACAAACCGCAAAAAAATAGTCGCAAAACGAC
	*** ***** ** ***** ***** ***** *****
E. c.	GAAACTACGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCT
V. c.	GAAACTACGCACTAGCAGCTTAATAACCTGCTCAGAGCCCTTCTCTCCCT
	***** ***** ***** ***** ***** ***** *****
E. c.	AGCCTCCGCTCTTAGGACGGGGAT - CAAGAGAGGTCAACCCAAAGAGA
V. c.	AGCTTCCGCTTGTAAGACGGGGAATCAGGAAGGTCAACCAAAATCAAGC
	*** ***** ** ***** ** ***** ***** **
E. c.	TCGCGTGGAAGCCCT - GCCTG - GGGTTGAAGCGTTAAACTTAATCAGGC
V. c.	TGGCGTGGAATCCCCCACCTGAGGGATGAAGCGCGAGATCTAATTCAGGT
	* ***** ** ***** *** ***** * * * * *
E. c.	TAGTTGTAGTGCGGTGTCCGTCCGACGTGGCAAGCGAATGTAAAGAC
V. c.	TAGCCATTCGTTAGCGGTGTCCGTTCGCGAGCGGTG - GTGAAATTAAGAT
	*** * * ***** ** ***** ** * * * * *
E. c.	TGACTAAGCATGTAGTACCGAGGATGTAGGAATTTTCGGACGCGGGTTCAA
V. c.	CGACTAAGCATGTAGTACCAAGATGAATGGTTTTCGGACGCGGGTTCAA
	***** ***** * ***** * ***** ***** *****
E. c.	CTCCCGCCAGCTCCACCAAAATTCCTCCA
V. c.	CTCCCCCAGCTCCACCA-----
	***** *****

FIG. 1

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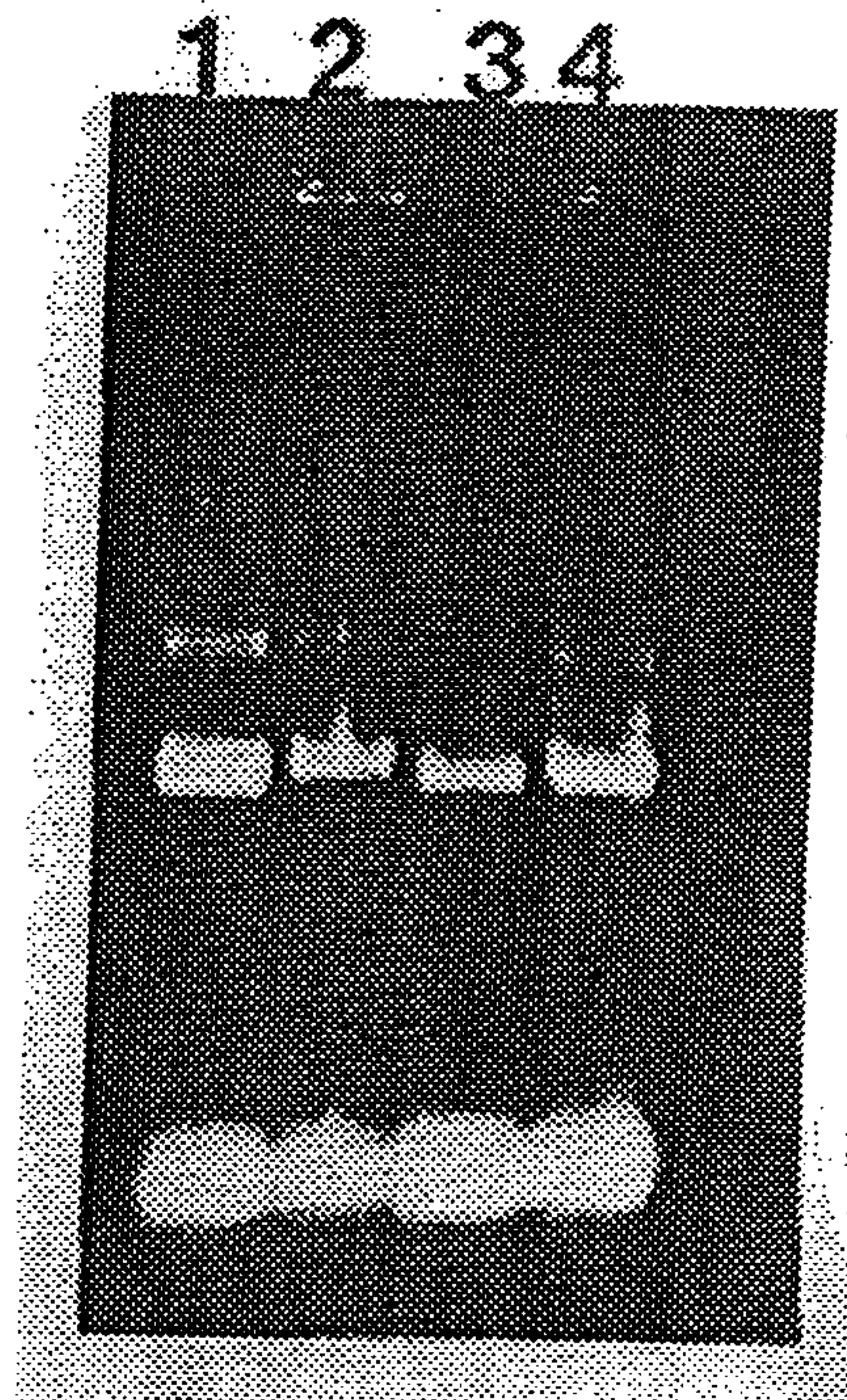


FIG. 2

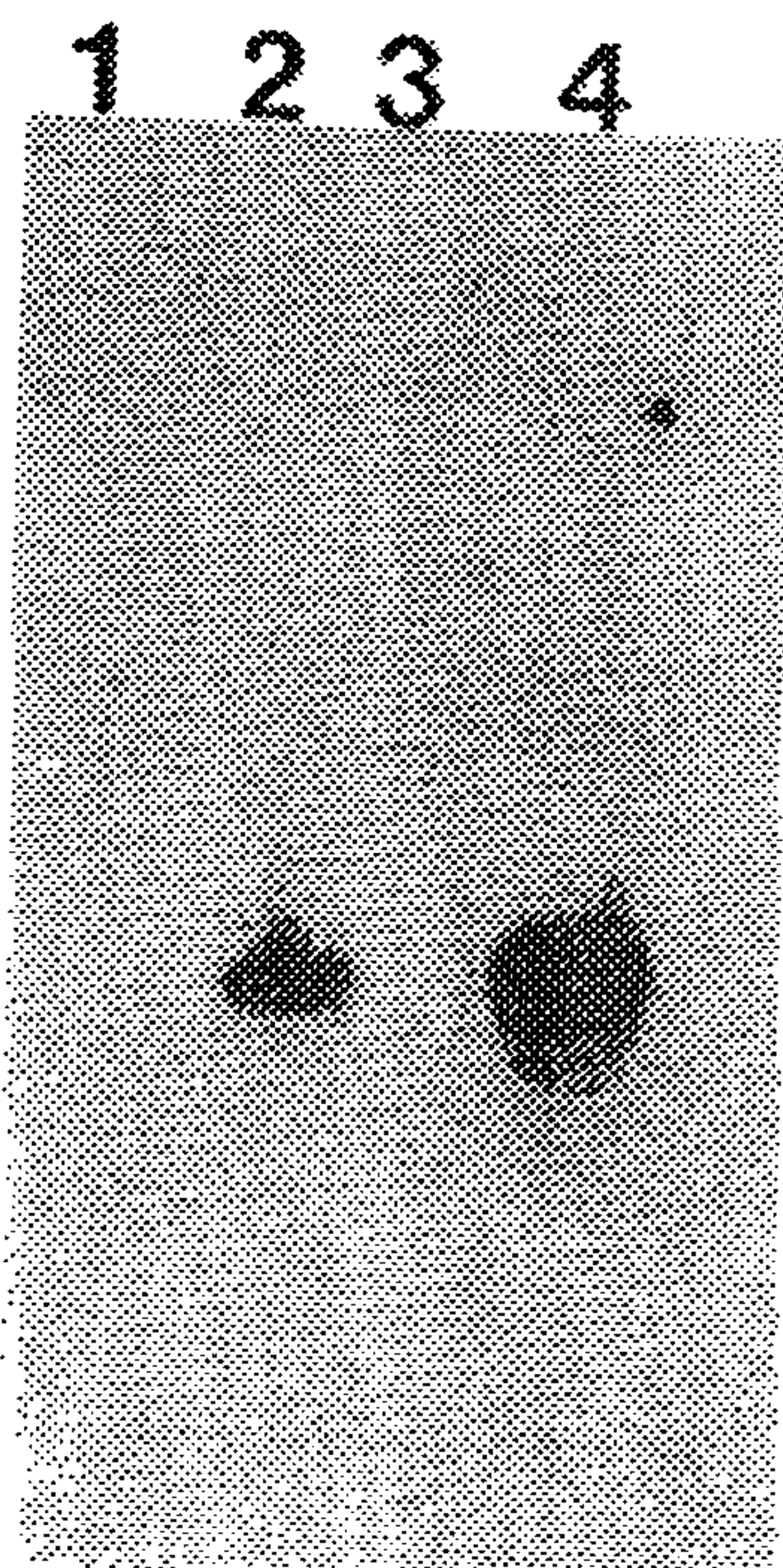


FIG. 3

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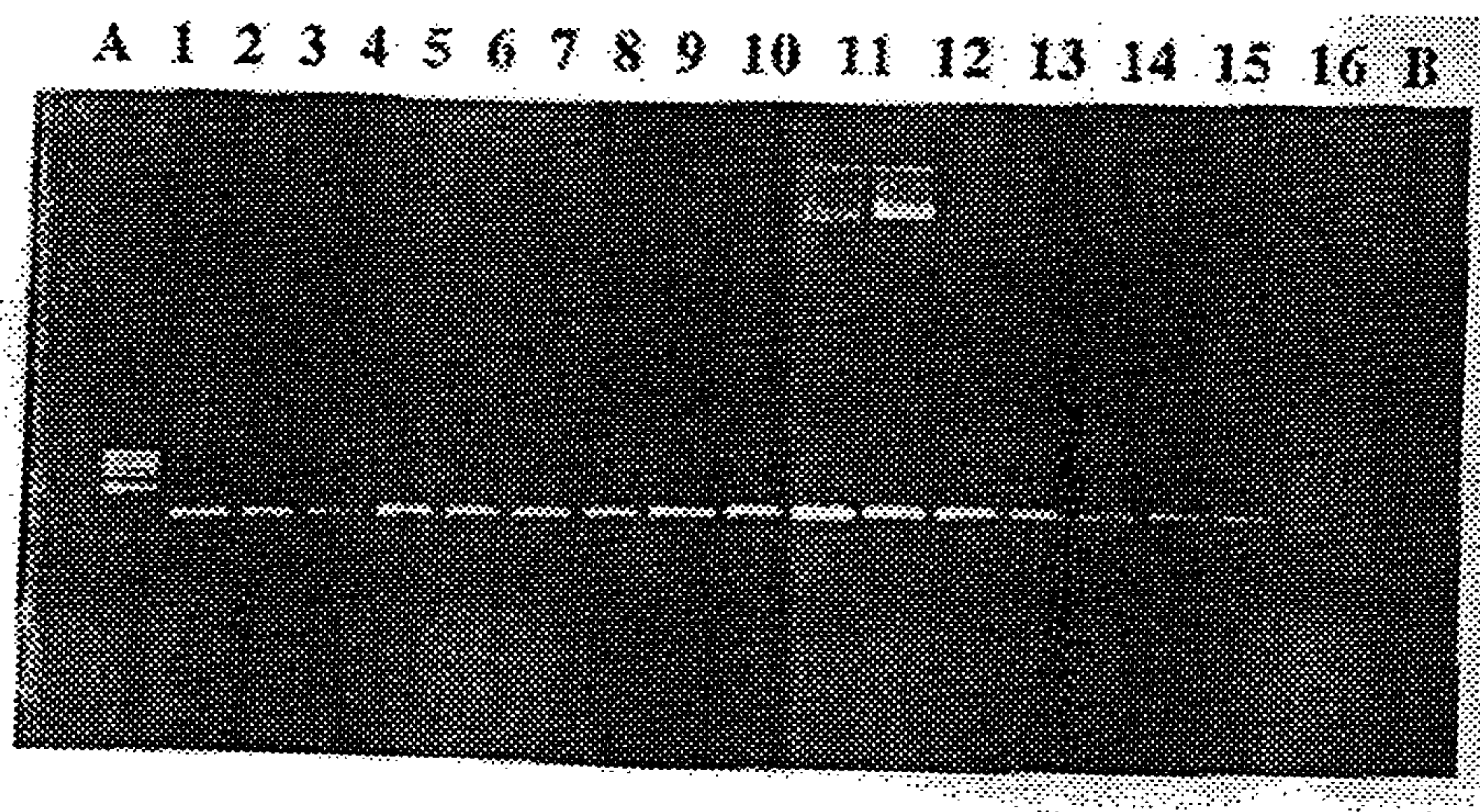


FIG. 4

L.m.	ACAGGGATAGTTCGAGCTTGAGTTGCCGAGTCGGGGGATCGTCCTCGTTA
L.i.	ACAGGGATAGTTCGAGCTTGAGTTGCCGAGTCGGGGGATCGTCCTCGTTA
L.mu.	ACAGGGATAGTTCGAGCTTGAGTTGCCGAGTCGGGGGATCGTCCTCGTTA
L.w.	ACAGGGATAGTTCGAGCTTGAGTTGCCGAGTCGGGGGATCGTCCTCGTTA
L.g.	ACAGGGATAGTTCGAGCTTGAGTTGCCGAGTCGGGGGATCGGCC-CGTCA *****
	Ltm1
L.m.	TCAACGTC AAAGCCCAATAAATACTGG CAAAGAAAACAACAACCTAGCTTT
L.i.	TCAACGTC AAAGCCCAATAAATACTGG CAAAGAAAACAACAACCTAGCTTT
L.mu.	TCAACGTC AAAGCCCAATAAATACTGG CAAAGAAAACAACAACCTAGCTTT
L.w.	TCAACGTC AAAGCCCAATAAATACTGG CAAAGAAAACAACAACCTAGCTTT
L.g.	TCAACGTC AAAGCCCAATAAATACTGG CAAACAAAACAACAATTAGCTTT *****
L.m.	CGCTGCCCTAATAAGCAGTA-GCATAGCTGATCCTCCGTGCATCGCCCATG
L.i.	CGCTGCCCTAATAAGCAGTA-GCATAGCTGATCCTCCGTGCATCGCCCATG
L.mu.	CGCTGCCCTAATAAGCAGTA-GCATAGCTGATCCTCCGTGCATCGCCCATG
L.w.	CGCTGCCCTAATAAGCAGTA-GCATAGCTGATCCTCCGTGCATCGCCCATG
L.g.	CGCTGCCCTAATA-GCAGTCTGAATAGCTGATCCTCCGTGCATCACCCATG *****
	Lgtm
L.m.	TG CTACGGTAAGGGTCTCAC TCT-AAGTGGGCTACACTAGTTAATCTCCG
L.i.	TG CTACGGTAAGGGTCTCAC TCT-AAGTGGGCTACACTAGTTAATCTCCG
L.mu.	TG CTACGGTAAGGGTCTCAC TCT-AAGTGGGCTACACTAGTTAATCTCCG
L.w.	TG CTACGGTAAGGGTCTCAC TCT-AAGTGGGCTACACTGGCTAATCTCCG
L.g.	TG CTACGGTAAGGGTCTCAC TTTTAAGTGGGTTACGCTGGCTTATCTCCG ** *****

FIG. 5A

L.m.
L.i.
L.mu.
L.w.
L.g.

L8tm

TCTGGGGTTAAATAGAAAGAGCTTAATCAGACTAGCTGAATGGAAGCCCTGT
TCTGAGGTTAAATAGAAAGAGCTTAATCAGACTAGCTGAATGGAAGCCCTGT
TCTGAGGTTAAATAGAAAGAGCTTAATGAGACTAGCTGAATGGAAGCCCTGT
TCTGAGGTTAGTTGGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCCTGT
TCTGGGGCAACGAGAGAGCATAAATCAGACTAGCTAGATAGAGCCCTGA
**** ** * ***** **** * ** *

L.m.
L.i.
L.mu.
L.w.
L.g.

TACCGGGCCGATGTTATGCGAAATGCTAATACGGTGACTACGCTCGTAG
TACCGGGCTGATGTTATGCGAAATGCTAATACGGTGACTACGCTCGTAG
TACCGGGCTGATGTTATGCGAAATGCTAATACGGTGACTACGCTCGTAG
TACCGGGCCGATGTTATGCGAAATGCTAATACGGTGACTACGCTCGTAG
CGCCGGGCAGACATCTATGCGAAATCCAAATACGGCAACTACGCTCGTAG
***** ** * ***** * ***** *****

Ltm2	
ATATTT	AAGTGCCGATATTTCTGG
ATATTC	AAGTGCCGATATTTCTGG
ATATTC	AAGTGCCGATATTTCTGG
ATATTT	AAGTGCCGATATTTCTGG
ATGCTC	AAGTGCCGATATTTCTGG
** *	*****

FIG. 5B

B.s.
L.m.
ACAGGGATGGATCGAGCTTGAGCTGCGAGCCGAGAGG--CGATCTCGTAA
ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGATCGTCCTCGTTA
***** * ***** * * * * * * * * * * * * *

B.s.
L.m.
ACACGCACTTAAATATAACTGGCAAACTAACAGTTTAAACCAAAACGTA
TCA-ACG-TCAAAGCCAA-TAATA--ACTGGCAAGAAACAAACCTA
* *

B.s.
L.m.
GCATTAGCTGCCCTAATAAGC-GCAGCGAGACT---CTTCCTGACATTGCC
GCTTTCGCTGCCCTAATAAGCAGTAGCATAGCTGATCCTCCGTGCATCGCC
* *

B.s.
L.m.
TATGTGT--CTGTGAAGAGCACA-TCCAAGTAGGCTACGCTTGC--GTTC
CATGTGCTACGGTAAGGGTCTCACTCTAAGTGGGCTACACTAGTTAATCT
***** * * * * * * * * * * * * * * * * * * *

B.s.
L.m.
CCGTCTGAGAACGTA-AGAAGAGATGAA-CAGACTAGCTCTCGGAAGGCC
CCGTCTGGGGTTAAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCC
***** * * * * * * * * * * * * * * * * * * *

B.s.
L.m.
CGCCCCAGGCAAGAGATGAGTGAAACCATAAATATGCAGGCTACGCTC
TGTTACCGGCCGATGTTTATGCCGAAAT-GCTAATACGGTGACTACGCTC
* *

B.s.
L.m.
G-AGACGCTTAAGTTAATCGATGTTTCTGG
GTAGATATTTAAGT--GCCGATATTTCTGG
* *

FIG. 6

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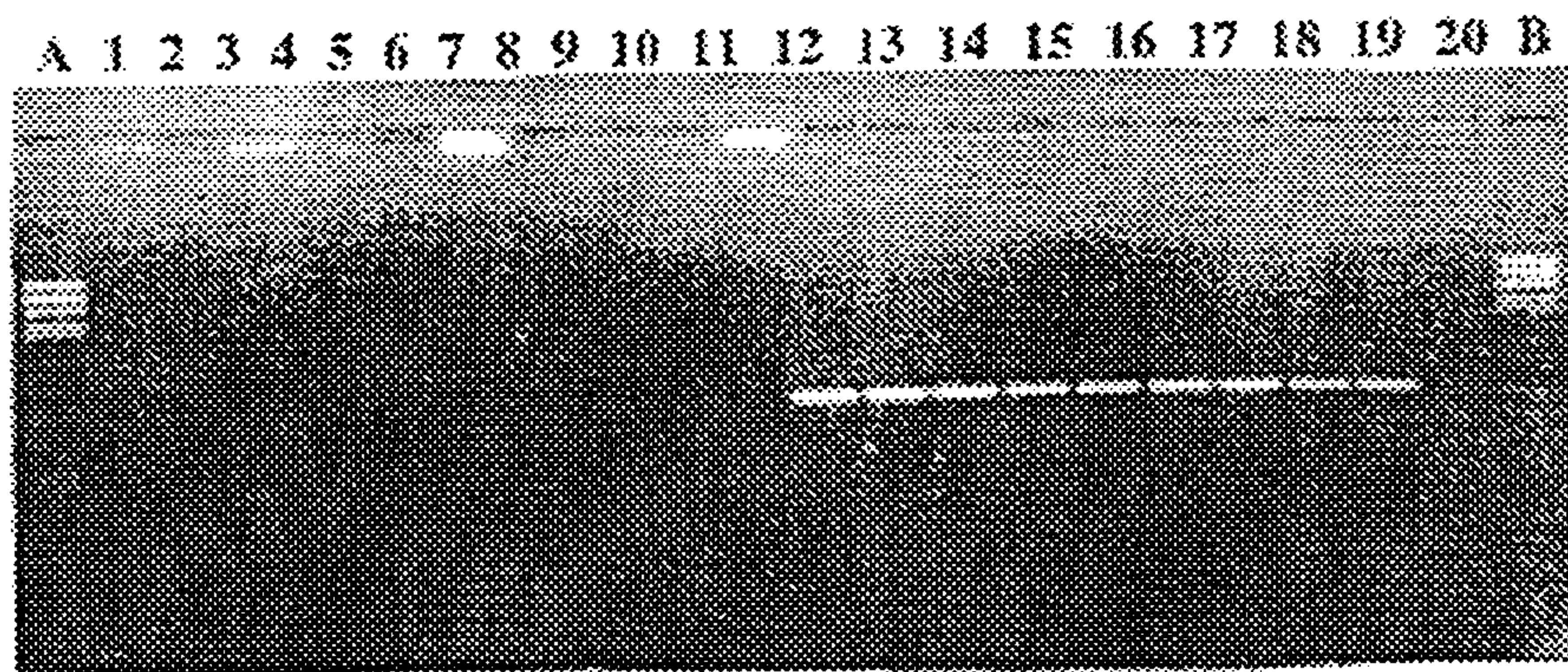


FIG. 7

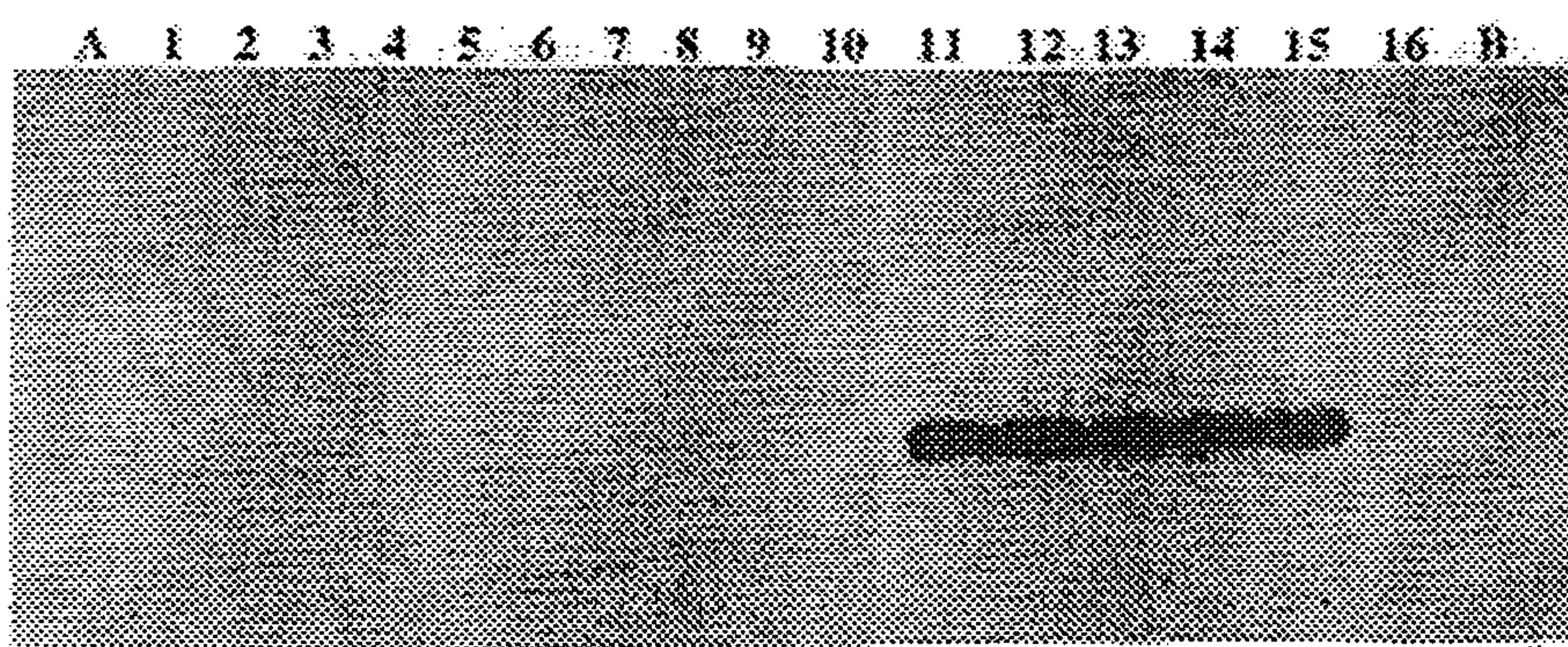


FIG. 8

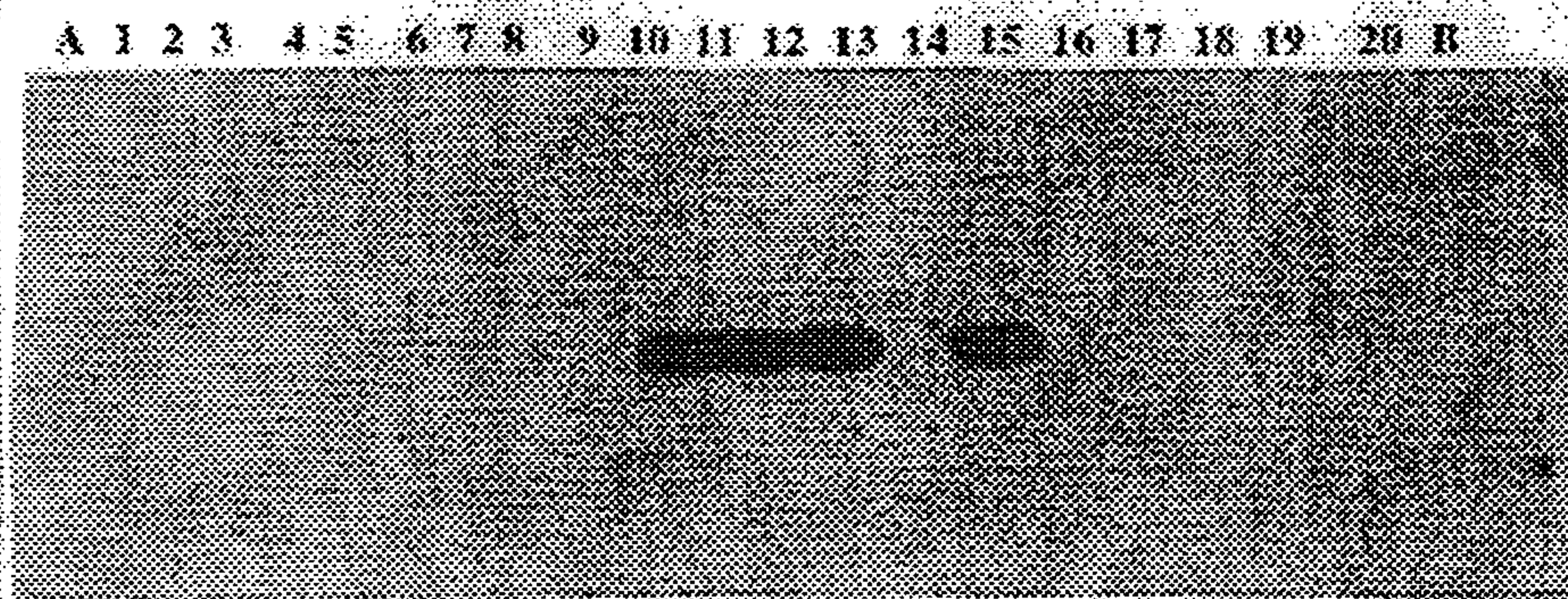


FIG. 9

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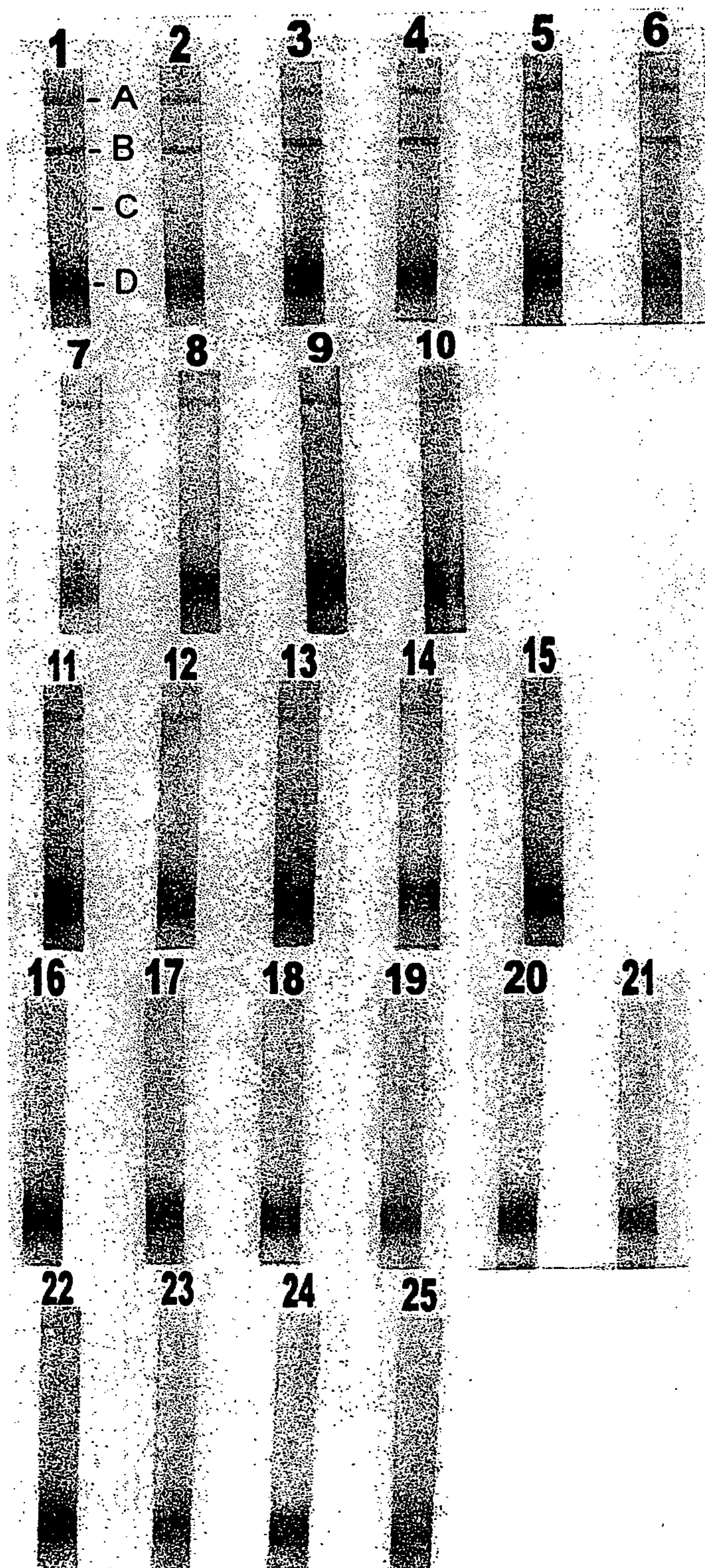


FIG. 10

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Ct 1	GGGGGTGTAAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCATGCCGGAG
Ct 2	GGGGGTGTAAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCATGCCGGAG

Ct 1	GGCGTTGGCTGGCCTCCTAAAGCCGACAAACAATAATGCCGAACCT
Ct 2	GGCGTTGGCTGGCCTCCTAAAGCCGACAAACAATAATGCCGAACCT

Ct 1	AAGGCTGAATGCCGAATTATCAGCTTCGCTGATCTCGAAGATCTAAGAGT
Ct 2	AAGGCTGAATGCCGAATTATCAGCTTCGCTGATCTTAATGATCTAAGAGT

Ct 1	AGCTGCTTAATTAGCAAAGTTGTTACCTAAATACGGGTGACCCGGTGTC
Ct 2	TGCTGCTTAATTAGCAAAGTTGTTACCTAAGTACTGGTAACCCGGTGTC

Ct 1	GCGAGCTCCACCAGAGGTTTTCGAAACACCGTCATGTATCTGGTTAGAAC
Ct 2	GCGAGCTCCACCAGAGGTTTTCGAAACGCGTCATTATCTGGTTAGAAAT

FIG. 11A

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Ct1	TTAGGTCCTTTAATTCTCGAGGAAATGAGTTTGAAATTTAATGAGAGTCG
Ct2	TAGGGCCCTTTTAACTCTCAAGGAACTAATTTGAAATTTTAATGAGAGTCG
	* ** * ***** ** * ***** ***** *
Ct1	TTAGTCTCTATAGGGGTTTCTAGCTGAGGAGACATAACGTATAGTAC-CT
Ct2	TTGGTCTCTATAGAGGTTTCTAGCTGAGGAGATATAACGTAAATATTCT
	** ***** ***** ***** * ** *
Ct1	AGGAACTAAGCATGTAGAGGTTAGCGGGAGTTTACTAAGGACGAGAGTT
Ct2	AGAAACTAAGCATGTAGAGGTTAGCGGGAGTTTACTAAGGACGAGAGTT
	** ***** ***** ***** ***** *
Ct1	CGACTCTCTCCACCTCCACCA
Ct2	CGAATCTCTCCACCTCCACCA
	** ***** *

FIG. 11B

HP1
HP2

AGATTTC TTGTCGCGCAGATAGCATGCCAAGCGCTGCTTGTA AACAGCA
AGATTTC TTGTCGCGCAGATAGCATGCCAAGCGCTGCTTGTA AACAGCA

HP1
HP2

ACAAAATACTGTAAACAACACAGATTACGCTCCAGCTTACGCTAAAGC
ACAAAATACTGTAAACAACACAGATTACGCTCCAGCTTACGCTAAAGC

HP1
HP2

TCCGTGAGTTAATCTCCTTTTGGAGCTGGACTGATTAGAA TTTCTAGCGT
TCCGTGAGTTAATCTCCTTTTGGAGCTGGACTGATTAGAA TTTCTAGCGT

HP1
HP2

TTTAATCGCTCCATAACCTTAAGCTAGACGCTTTTAAAGGTGTTTCGCC
TTTAATCGCTCCATAACCTTAAGCTAGACGCTTTTAAAGGTGTTTCGCC

HP1
HP2

TTTTAAACTAAGAAACAAGAACTCTTGAAACTATCTTAAGGTTTTAGAAA
TTTTAAACTAAGAAACAAGAACTCTTGAAACTATCTCAAGGTTTTAGAAA

HP1
HP2

GTTGGACCAGAGCTAGTTTTTAAGGCTAAAACTAACCAATTTTCTAAGC
GTTGGACCAGAGCTAGTTTTTAAGGCTAAAACTAACCAATTTTCTAAGC

HP1
HP2

ATTGTAGAAGTTTGTTAGGGCAAGATTTTGTGGACTGGGG
ATTGTAGAAGTTTGTTAGGGCAAGATTTTGTGGACTGGGG

FIG. 12

Mc1	ACATAATGCTGATAGACAACACAGTAGCATTGGGGTATGCCCCCTTACAGCG	12/20
Mc2	ACATAATGCTGATAGACAACACAGTAGCATTGGGGTATGCCCCCTTACAGCG	
Mc1	CTAGGTTCAATAACCGACAAAGAAATAACGAAGTGTGGTAGAACCAAA	
Mc2	CTAGGTTCAATAACCGACAAAGAAATAACGAAGTGTGGTAGATCCAAA	
Mc1	TTTGATCATTAACCAACAAGCAAGTGTTAACTTTGCTTTTGCATAAGTAG	
Mc2	TTTGATCATTAACCAACAAGCAAGTGTTAACTTTGCTTTTGCATAAGTAG	
Mc1	ATACTAAAGCTACAGCTGGTGAAATAGTCATAGTTTGCTAGCTGTCTAGT	
Mc2	ATACTAAAGCTACAGCTGGTGAAATAGTCATAGTTTGCTAGCTGTCTAGT	
Mc1	TTATGACTCGAGGTAAATCGTTCAATTTAAACCTTTAAATAATAGAACTTG	
Mc2	TTATGACTCGAGGTAAATCGTTCAATTTAAACCTTTAAATAATAGAACTTG	
Mc1	TTGTTTCCATGATTGTTTGTGATCAATTGGAAACAAGACAAATAATCCAC	
Mc2	TTGTTTCCATGATTGTTTGTGATCAATTGGAAACAAGACAAATAATCCAC	
Mc1	AAACTAAATGTAGAAGCTGTTTGTGTCTCTTTATGGAAACGGGTTTC	
Mc2	AAACTAAATGTAGAAGCTGTTTGTGTCTCTTTATGGAAACGGGTTTC	

FIG. 13

Ng1
Ng2

GGGGTTGCGAAGCAGATGCGGGCATACCGGGTCTCAGATTCCCGTAA
GGGGTTGCGAAGCAGATGCGGGCATACCGGGTCTCAGATTCCCGTAA

Ng1
Ng2

ACACTGAATTCAAAATAGTCGCAAAACGACGAAACTTACGCTTTAGCCGCTT
ACACTGAATTCAAAATAGTCGCAAAACGACGAAACTTACGCTTTAGCCGCTT

Ng1
Ng2

AAGGCTAGCCGTTGCAGCAGTCGGTCAATGGGCTGTGTGGGAAAGCCAC
AAGGCTAGCCGTTGCAGCAGTCGGTCAATGGGCTGTGTGGTGAAGCCAC

Ng1
Ng2

CGCAACGTCATCTTACATTGACTGGTTTCCAGCCGGTTACTTGGCAGGA
CGCAACGTCATCTTACATTGACTGGTTTCCAGCCGGTTACTTGGCAGGA

Ng1
Ng2

AATAAGACTTAAGGTAAC TGGTTTCCAAAGGCCCTGTGGTCGGCATGAT
AATAAGACTTAAGGTAAC TGGTTTCCAAAGGCCCTGTGGTCGGCATGAT

Ng1
Ng2

GGAAATAAGATTTTCAAATAGACACAATAAGTATGTAGAACGCTTTGTA
GGAAATAAGATTTTCAAATAGACACAATAAGTATGTAGAACGCTTTGTA

Ng1
Ng2

GAGGACTTTCGGACGGGG
GAGGACTTTCGGACGGGG

FIG. 14

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L.m1	CAAAGAAAACAAACCTAGCTTTCGGCTGCCCTAATAAGCAGTAGCATAGC
L.m2	CAAAGAAAACAAACCTAGCTTTCGGCTGCCCTAATAAGCAGTAGCATAGC *****
L.m1	TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT
L.m2	TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT *****
L.m1	GGGCTACACTAGTTAATCTCCGTCTGGGGTTAAATAGAAGAGCTTAATCA
L.m2	GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCA *****
L.m1	GACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTATGCCGAAATGCT
L.m2	GACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTATGCCGAAATGCT *****
L.m1	AATACGGTGACTACGCTCGTAGATATTT
L.m2	AATACGGTGACTACGCTCGTAGATATTT *****

FIG. 15

L.m1	CAAAGAAACAAACCTAGCTTTTCGCTGCCCTAATAAGCAGTAGCATAGC
L.m2	CAAAGAAACAAACCTAGCTTTTCGCTGCCCTAATAAGCAGTAGCATAGC
L.i	CAAAGAAACAAACCTAGCTTTTCGCTGCCCTAATAAGCAGTAGCATAGC *****
L.m1	TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGTCTCACTCTAAGT
L.m2	TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGTCTCACTCTAAGT
L.i	TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGTCTCACTCTAAGT *****
L.m1	GGGCTACACTAGTTAATCTCCGTCTGGGGTTAAATAGAAGAGCTTAATCA
L.m2	GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCA
L.i	GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCA *****
L.m1	GACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCCGAAATGCT
L.m2	GACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCCGAAATGCT
L.i	GACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTATGCCGAAATGCT *****
L.m1	AATACGGTGACTACGCTCGTAGATATTT
L.m2	AATACGGTGACTACGCTCGTAGATATTT
L.i	AATACGGTGACTACGCTCGTAGATATTC *****

FIG. 16

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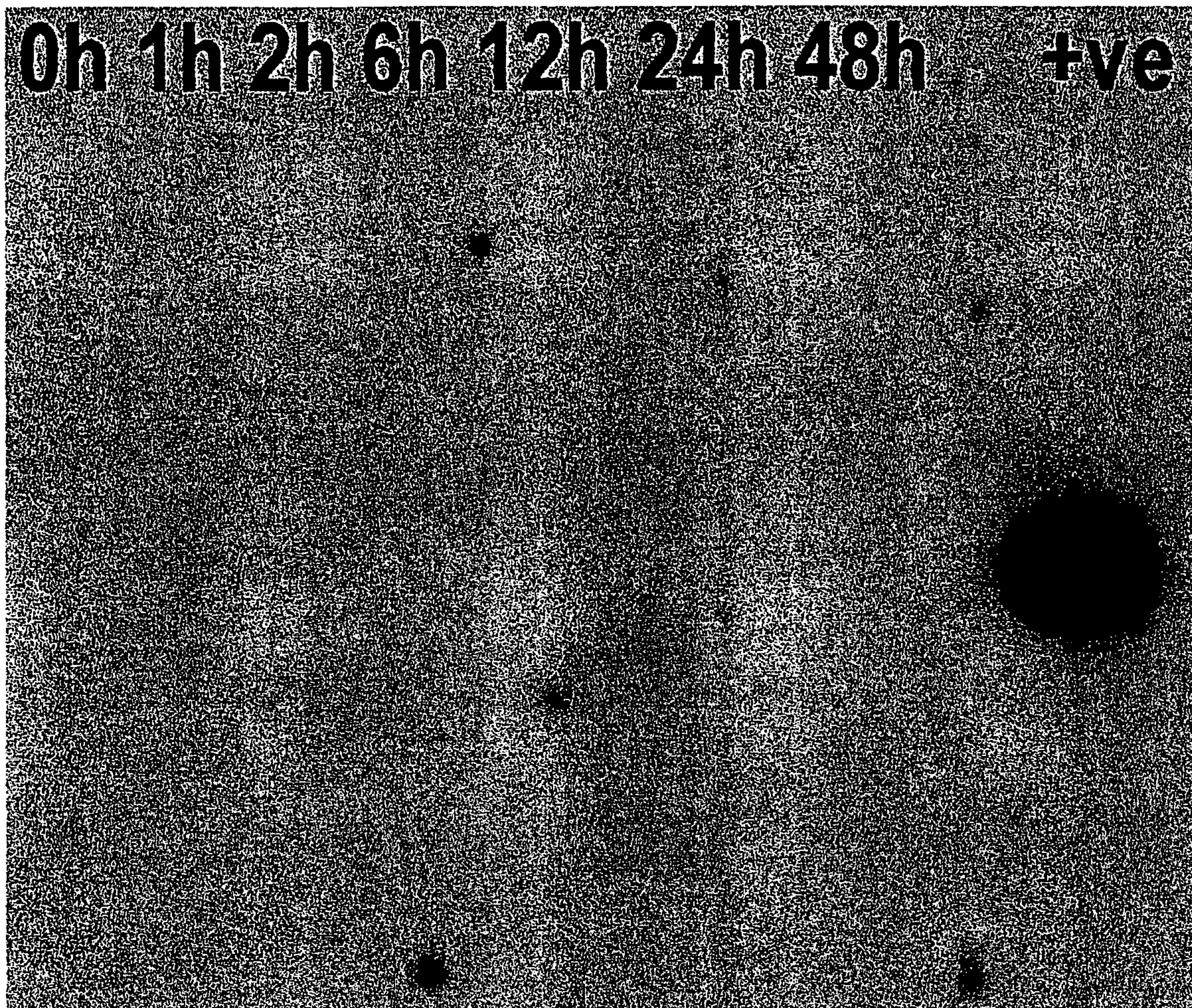


FIG. 17

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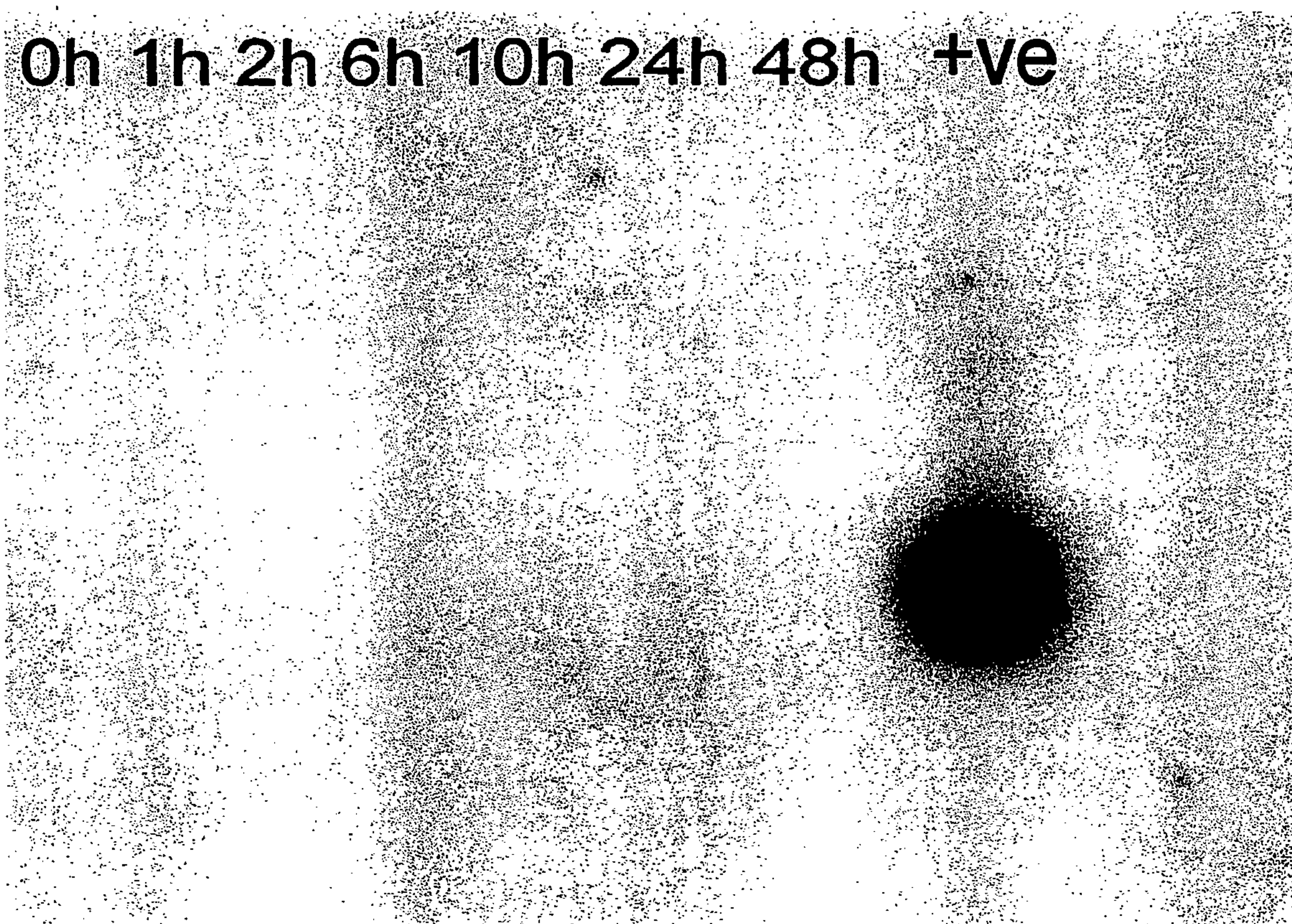


FIG. 18

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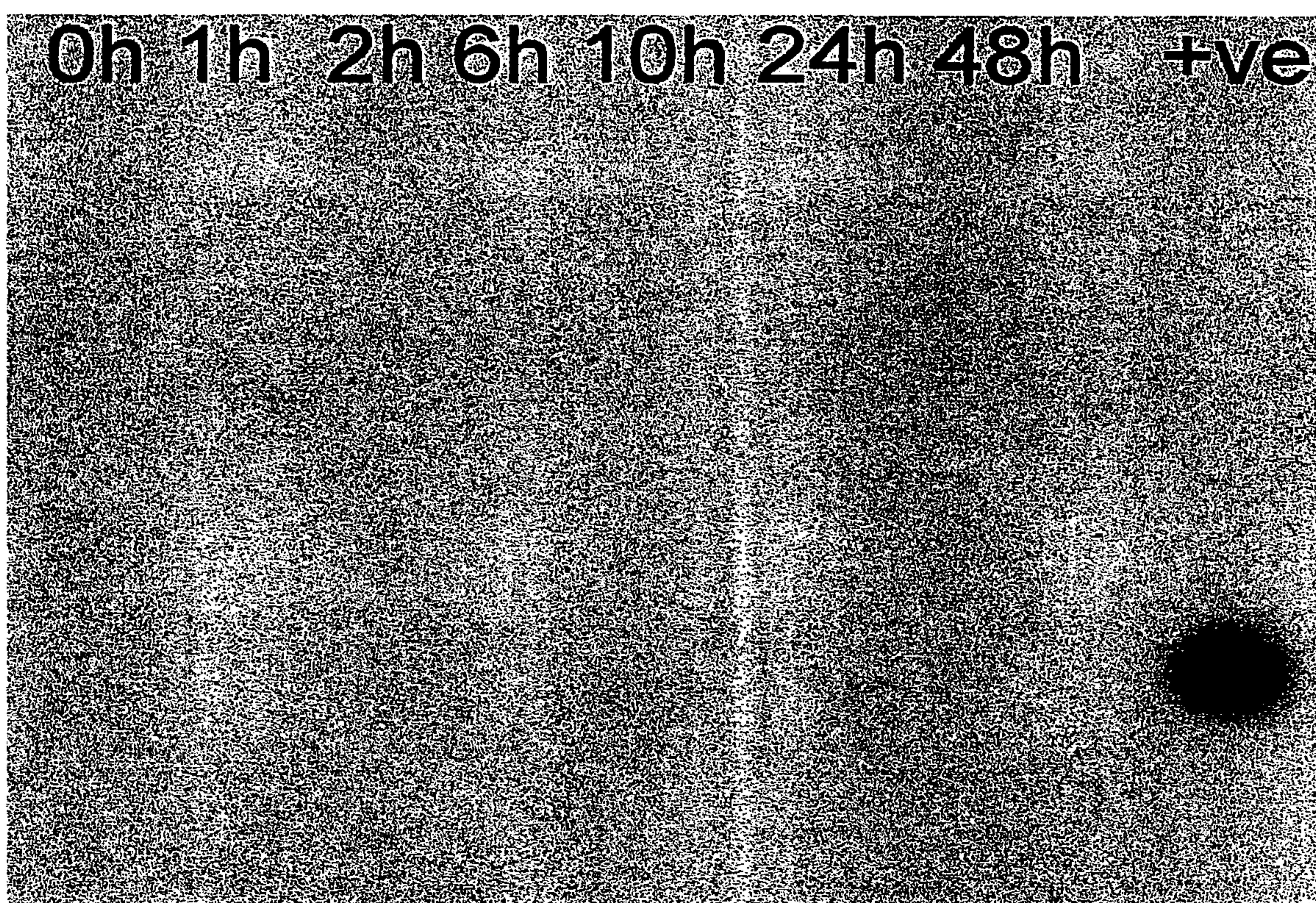


FIG. 19

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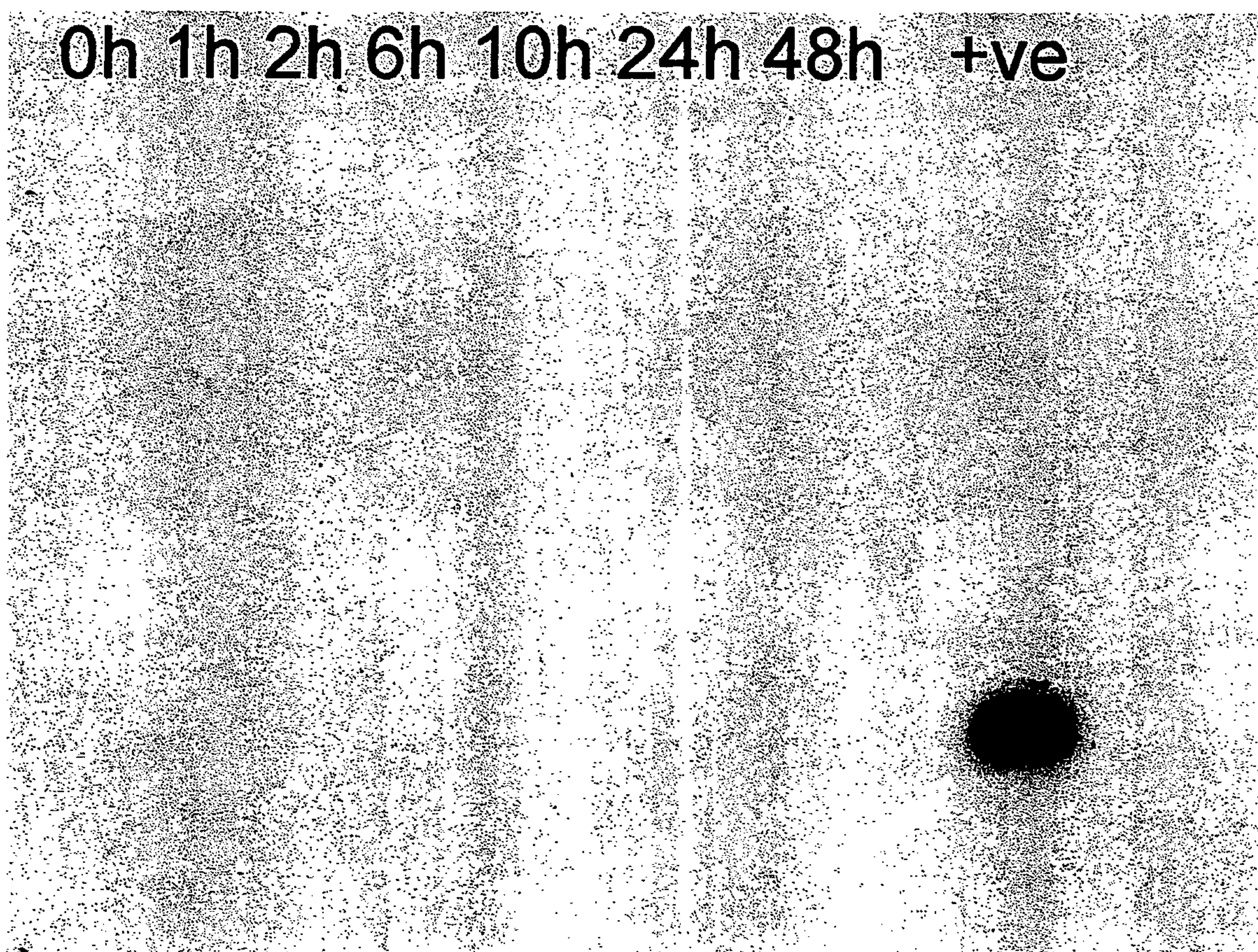


FIG. 20

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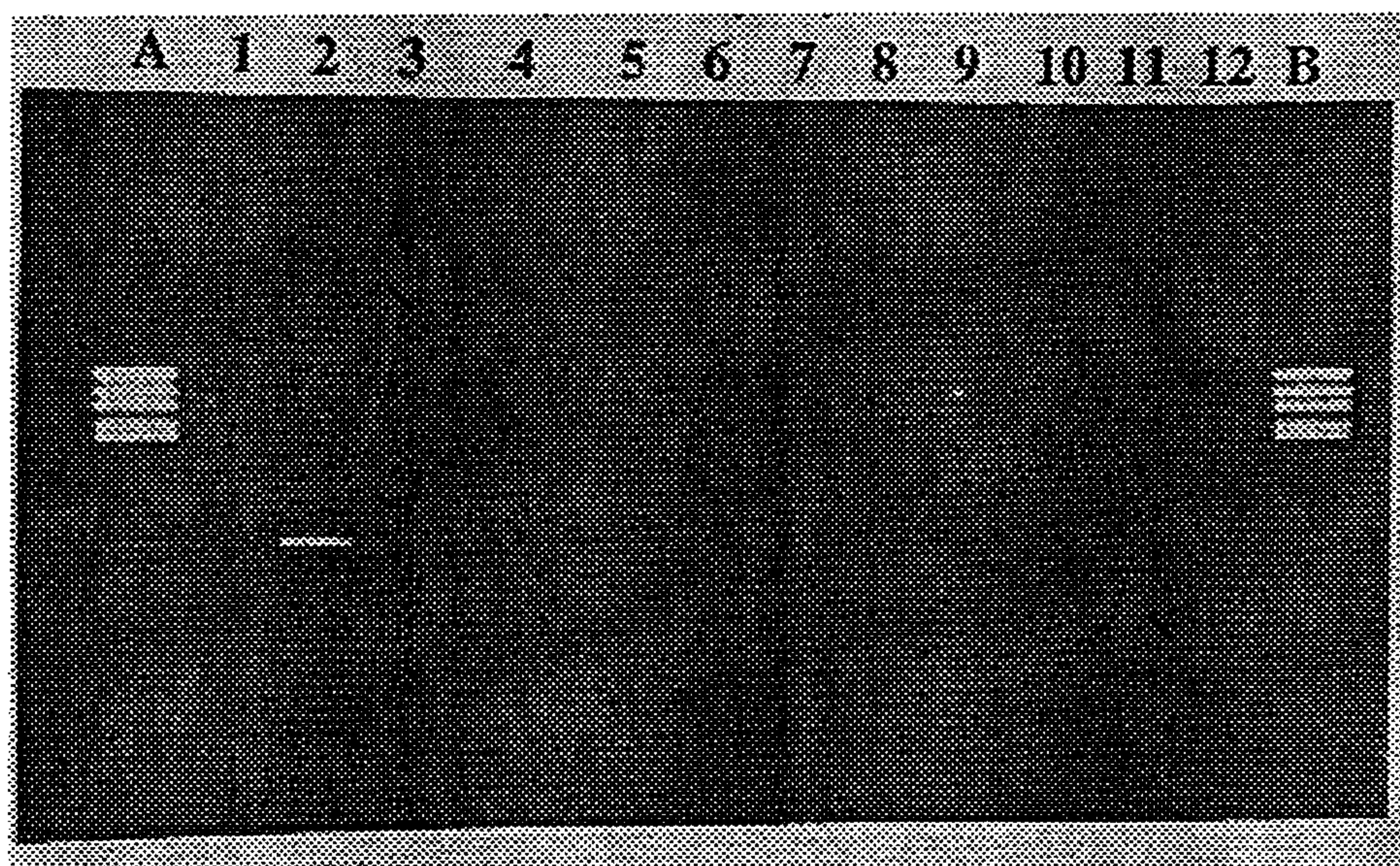


FIG. 21